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## SEQUENCE LISTING

<110> MURDIN, Andrew D.; OOMEN, Raymond P; and WANG, Joe

<120> Chlamydia antigens and corresponding DNA fragments and uses thereof

10 <130> 77813-51

<140> PCT/CA99/00992

<141> 1999-10-28

<150> US 60/106034

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 30 acc aaa ggt tcg aac tta gca aga cag gct ggt att gtt cag gcc tca 2415  
 Thr Lys Gly Ser Asn Leu Ala Arg Gln Ala Gly Ile Val Gln Ala Ser  
 790 795 800 805  
 ggt ttt cga tct ttg gga gct gca gca gag ctt ttc ggg aac ttt ggc 2463  
 Gly Phe Arg Ser Leu Gly Ala Ala Ala Glu Leu Phe Gly Asn Phe Gly  
 810 815 820  
 ttt gaa tgg cgg gga tct tct cgt agc tat aat gta gat gcg ggt agc 2511  
 Phe Glu Trp Arg Gly Ser Ser Arg Ser Tyr Asn Val Asp Ala Gly Ser  
 825 830 835  
 40 aaa atc aaa ttt 2523  
 Lys Ile Lys Phe  
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 <212> DNA  
 <213> Chlamydia pneumoniae  
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 50 <221> CDS  
 <222> (101)..(835)  
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 agtacaacag cctgttgctg catcgctcagt gccttcctac atg ccc cca ctg aat 115  
 Met Pro Pro Leu Asn  
 1 5

60

230	235	240	245
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taaggacacg tgccgtgtta gcattttttcg caactagttt caaatctgtt cttttttgagt 895  
 actcctacca atcattatta cttattttga ttgtttcggc acctcccatc atcttagctt 955  
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 10 <212> PRT  
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<220>  
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 <222> (188)..(197)

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tgaggtaa at cagcctcaaa gatactacgc catagtaa atg aag ttt ttt agc 115  
 Met Lys Phe Phe Ser  
 1 5

tta att ttt aaa gat gat gat gtc tcc cca aat aag aag gtt tta tct 163  
 Leu Ile Phe Lys Asp Asp Asp Val Ser Pro Asn Lys Lys Val Leu Ser  
 10 15 20

cct gaa gct ttc tct gct ttc ctt gat gcc aaa gag ctg tta gaa aaa 211  
 Pro Glu Ala Phe Ser Ala Phe Leu Asp Ala Lys Glu Leu Leu Glu Lys  
 25 30 35

aca aaa gcc gat agc gaa gcc tat gtt gca gag aca gaa caa aag tgt 259  
 Thr Lys Ala Asp Ser Glu Ala Tyr Val Ala Glu Thr Glu Gln Lys Cys  
 40 45 50

gca caa att cgt caa gaa gct aaa gat caa gga ttt aaa gag gga tct 307  
 Ala Gln Ile Arg Gln Glu Ala Lys Asp Gln Gly Phe Lys Glu Gly Ser  
 55 60 65

gaa tcc tgg agc aag caa att gct ttc tta gaa gaa gaa act aaa aat 355  
 Glu Ser Trp Ser Lys Gln Ile Ala Phe Leu Glu Glu Glu Thr Lys Asn  
 70 75 80 85

cta cgc ata aga gta cgc gag gcc ttg gtt cct ctg gca att gcg agt 403  
 Leu Arg Ile Arg Val Arg Glu Ala Leu Val Pro Leu Ala Ile Ala Ser  
 90 95 100

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gtg agg aaa atc att ggg aag gaa ctc gaa tta cat cct gaa act att 451  
 Val Arg Lys Ile Ile Gly Lys Glu Leu Glu Leu His Pro Glu Thr Ile  
 105 110 115

gtc tct att att tct caa gca ttg aaa gag ctc aca caa aat aaa cat 499  
 Val Ser Ile Ile Ser Gln Ala Leu Lys Glu Leu Thr Gln Asn Lys His  
 120 125 130

10

atc att atc tct gtc aat ccc aaa gat tta cct ctt gtt gag aaa agt 547  
 Ile Ile Ile Ser Val Asn Pro Lys Asp Leu Pro Leu Val Glu Lys Ser  
 135 140 145

cgt cct gaa ctc aag aac atc gtg gag tat gct gac tcc tta att ctt 595  
 Arg Pro Glu Leu Lys Asn Ile Val Glu Tyr Ala Asp Ser Leu Ile Leu  
 150 155 160 165

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aca gca aaa cct gat gtt act cct ggg ggt tgc att atc gag act gaa 643  
 Thr Ala Lys Pro Asp Val Thr Pro Gly Gly Cys Ile Ile Glu Thr Glu  
 170 175 180

gca ggg atc atc aat gcg cag ctt gat gta caa tta gat gcc tta gaa 691  
 Ala Gly Ile Ile Asn Ala Gln Leu Asp Val Gln Leu Asp Ala Leu Glu  
 185 190 195

aaa gct ttc tcg act ata cta aaa gcg aag aac cct gta gac gag cca 739  
 Lys Ala Phe Ser Thr Ile Leu Lys Ala Lys Asn Pro Val Asp Glu Pro  
 200 205 210

30

tct gag act tca tca tcc acg gat tct tct tct tta tct aat gat cag 787  
 Ser Glu Thr Ser Ser Ser Thr Asp Ser Ser Ser Leu Ser Asn Asp Gln  
 215 220 225

gat aag aaa gaa taaaggatt cactattatg cgatccattt ttcgattttc 839  
 Asp Lys Lys Glu  
 230

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cctttgtttt tttacgctga gcgtctcatg ctgatttgct gacgccagtc tatatgaaaa 899  
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 60 <213> Chlamydia pneumoniae

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1066)

&lt;400&gt; 7

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10	tatggttcgt	cgatctat	ctttttgctt	gttctttcta	atg	aca	ttg	ctg	tgc	115							
					Met	Thr	Leu	Leu	Cys								
					1				5								
	tgt	aca	agc	tgt	aac	agc	agg	tct	cta	att	gtg	cac	ggg	ctt	cct	ggc	163
	Cys	Thr	Ser	Cys	Asn	Ser	Arg	Ser	Leu	Ile	Val	His	Gly	Leu	Pro	Gly	
					10					15				20			
	aga	gaa	gcg	aat	gag	att	gtg	gtg	ctt	ttg	gta	agc	aaa	ggg	gtg	gct	211
20	Arg	Glu	Ala	Asn	Glu	Ile	Val	Val	Leu	Leu	Val	Ser	Lys	Gly	Val	Ala	
				25					30					35			
	gca	caa	aaa	ttg	cct	caa	gct	gca	gcg	gct	aca	gcc	gga	gca	gct	act	259
	Ala	Gln	Lys	Leu	Pro	Gln	Ala	Ala	Ala	Ala	Thr	Ala	Gly	Ala	Ala	Thr	
			40				45					50					
	gag	caa	atg	tgg	gat	atc	gcg	gtt	ccg	tca	gca	caa	atc	aca	gag	gcc	307
	Glu	Gln	Met	Trp	Asp	Ile	Ala	Val	Pro	Ser	Ala	Gln	Ile	Thr	Glu	Ala	
		55				60					65						
30	ctt	gcc	att	cta	aat	caa	gcg	ggg	ctt	cca	cgt	atg	aaa	ggg	aca	agc	355
	Leu	Ala	Ile	Leu	Asn	Gln	Ala	Gly	Leu	Pro	Arg	Met	Lys	Gly	Thr	Ser	
	70					75				80					85		
	ctg	tta	gat	ctt	ttt	gca	aaa	caa	ggg	ctt	gtt	cct	tcc	gag	ctt	cag	403
	Leu	Leu	Asp	Leu	Phe	Ala	Lys	Gln	Gly	Leu	Val	Pro	Ser	Glu	Leu	Gln	
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	gaa	aaa	atc	cgt	tat	caa	gaa	ggc	tta	tca	gaa	cag	atg	gcc	tct	acg	451
40	Glu	Lys	Ile	Arg	Tyr	Gln	Glu	Gly	Leu	Ser	Glu	Gln	Met	Ala	Ser	Thr	
				105				110						115			
	att	aga	aaa	atg	gat	ggc	gtt	gtc	gat	gcc	tca	gta	cag	att	tcc	ttc	499
	Ile	Arg	Lys	Met	Asp	Gly	Val	Val	Asp	Ala	Ser	Val	Gln	Ile	Ser	Phe	
			120				125						130				
	act	aca	gaa	aat	gaa	gat	aat	ctt	cct	tta	aca	gcc	tct	gtg	tat	att	547
	Thr	Thr	Glu	Asn	Glu	Asp	Asn	Leu	Pro	Leu	Thr	Ala	Ser	Val	Tyr	Ile	
			135				140					145					
50	aag	cat	cga	ggg	gtt	ttg	gac	aat	ccg	aac	agc	att	atg	gtt	tcc	aaa	595
	Lys	His	Arg	Gly	Val	Leu	Asp	Asn	Pro	Asn	Ser	Ile	Met	Val	Ser	Lys	
					155				160							165	
	att	aag	cgc	ctt	att	gca	agt	gct	gtt	cca	gga	ctt	gtg	cca	gag	aac	643
	Ile	Lys	Arg	Leu	Ile	Ala	Ser	Ala	Val	Pro	Gly	Leu	Val	Pro	Glu	Asn	
				170					175						180		
	gtc	tct	gta	gtg	agc	gat	cgc	gca	gct	tat	agt	gat	att	aca	att	aat	691
60	Val	Ser	Val	Val	Ser	Asp	Arg	Ala	Ala	Tyr	Ser	Asp	Ile	Thr	Ile	Asn	
			185					190					195				

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ggt cct tgg gga tta aca gaa gaa atc gat tat gtt tct gtt tgg ggt 739  
 Gly Pro Trp Gly Leu Thr Glu Glu Ile Asp Tyr Val Ser Val Trp Gly  
 200 205 210

att att ctt gcg aag tct tcg ctc acc aaa ttc cgt ctc att ttt tat 787  
 Ile Ile Leu Ala Lys Ser Ser Leu Thr Lys Phe Arg Leu Ile Phe Tyr  
 215 220 225

10

gtc ttg att ctc att tta ttt gtt att tct tgt ggt ctc ctt tgg gtc 835  
 Val Leu Ile Leu Ile Leu Phe Val Ile Ser Cys Gly Leu Leu Trp Val  
 230 235 240 245

att tgg aaa act cat act ctc att atg act atg gga ggt aca aaa ggg 883  
 Ile Trp Lys Thr His Thr Leu Ile Met Thr Met Gly Gly Thr Lys Gly  
 250 255 260

20

ttc ttc aac cct aca cca tat aca aag aat gcc ttg gaa gcc aag aaa 931  
 Phe Phe Asn Pro Thr Pro Tyr Thr Lys Asn Ala Leu Glu Ala Lys Lys  
 265 270 275

gcc gag gga gca gct gct gac aaa gag aaa aaa gaa gat gca gat tca 979  
 Ala Glu Gly Ala Ala Ala Asp Lys Glu Lys Lys Glu Asp Ala Asp Ser  
 280 285 290

cag ggg gaa agc aaa aat gcg gaa acc agt gat aaa gac tct agt gat 1027  
 Gln Gly Glu Ser Lys Asn Ala Glu Thr Ser Asp Lys Asp Ser Ser Asp  
 295 300 305

30

aaa gat gct cca gaa gga agc aat gaa att gag ggt gct tagtgactgc 1076  
 Lys Asp Ala Pro Glu Gly Ser Asn Glu Ile Glu Gly Ala  
 310 315 320

caacactttt ggaactctag acatcttgat gaagcactcc aaggaagatg acctctccag 1136  
 gtttcttctt aaaaatcttc ttgttgaatc tcctcatccc gaagaaatcc ctttaaaatc 1196  
 tttta 1200

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<210> 9  
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ttttcctgta tttctagggt atcagaaaag agaaggagtt atg aca att aga gtc 115  
 Met Thr Ile Arg Val  
 1 5

10 cga aac ctt gcc tac tct gta aat aag aaa aag att cta gat ggt gta 163  
 Arg Asn Leu Ala Tyr Ser Val Asn Lys Lys Lys Ile Leu Asp Gly Val  
 10 15 20

act ttt tct tta gag cga ggg cac att aca ctg ttt gtt ggg aag agt 211  
 Thr Phe Ser Leu Glu Arg Gly His Ile Thr Leu Phe Val Gly Lys Ser  
 25 30 35

20 ggt tca gga aaa aca atg att tta cgt gct ttg gcg ggc tta gtc cag 259  
 Gly Ser Gly Lys Thr Met Ile Leu Arg Ala Leu Ala Gly Leu Val Gln  
 40 45 50

ccc act caa gga gat att tgg att gaa ggg gag gct cca gct cta gtt 307  
 Pro Thr Gln Gly Asp Ile Trp Ile Glu Gly Glu Ala Pro Ala Leu Val  
 55 60 65

ttc caa caa ccc gag tta ttt tcc cat atg aca gta tta gga aat tgc 355  
 Phe Gln Gln Pro Glu Leu Phe Ser His Met Thr Val Leu Gly Asn Cys  
 70 75 80 85

30 acc cat cca caa atc cat atc aag ggt cgt agt acc gaa gaa gct cga 403  
 Thr His Pro Gln Ile His Ile Lys Gly Arg Ser Thr Glu Glu Ala Arg  
 90 95 100

gaa aag gcg ttc gag ctt tta cat ttg ttg gat att gaa gag gtt gct 451  
 Glu Lys Ala Phe Glu Leu Leu His Leu Leu Asp Ile Glu Glu Val Ala  
 105 110 115

40 aag aat tat cct gac cag ctc tct ggg gga caa aaa caa cgt gtg gct 499  
 Lys Asn Tyr Pro Asp Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Ala  
 120 125 130

att gta cgt tct tta tgt atg gat aaa cat aca tta ctt ttt gat gaa 547  
 Ile Val Arg Ser Leu Cys Met Asp Lys His Thr Leu Leu Phe Asp Glu  
 135 140 145

cct aca tcg gct tta gat cct ttt gct acg gca tcg ttc cga cat ctt 595  
 Pro Thr Ser Ala Leu Asp Pro Phe Ala Thr Ala Ser Phe Arg His Leu  
 150 155 160 165

50 tta gaa aca ctt cga gac cag gaa ctg act gta ggg tta act act cat 643  
 Leu Glu Thr Leu Arg Asp Gln Glu Leu Thr Val Gly Leu Thr Thr His  
 170 175 180

gac atg caa ttt gtt cat agt tgt ttg gat cgt atc tat ctt ata gat 691  
 Asp Met Gln Phe Val His Ser Cys Leu Asp Arg Ile Tyr Leu Ile Asp  
 185 190 195

60 caa gga act gtt gcg ggg gtc tat gac aag cgt gac gga gag ctc gat 739  
 Gln Gly Thr Val Ala Gly Val Tyr Asp Lys Arg Asp Gly Glu Leu Asp  
 200 205 210

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tct ggt cat cca tta tcg aaa tat atc cac tct gct caa taggactaca 788  
 Ser Gly His Pro Leu Ser Lys Tyr Ile His Ser Ala Gln  
           215                          220                          225

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 tg 850

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 <212> PRT  
 <213> Chlamydia pneumoniae

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 <222> (145)..(153)

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 <213> Chlamydia pneumoniae

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<220>  
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 <222> (101)..(1408)

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                                                   Met Lys Arg Pro Phe  
                                                   1                              5

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ttt acc tat cta tgc atc atc ttc tac gga tct tgt gca tcg tta tct 163  
 Phe Thr Tyr Leu Cys Ile Ile Phe Tyr Gly Ser Cys Ala Ser Leu Ser  
                               10                              15                              20

tta cat gca gga ctc tct ttc cca gaa gta cgt gga gct acg gct gct 211  
 Leu His Ala Gly Leu Ser Phe Pro Glu Val Arg Gly Ala Thr Ala Ala  
                               25                              30                              35

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gtt gtc cat gcc gac tct ggg aag gta ttc tat gat aaa gac ata gat 259  
 Val Val His Ala Asp Ser Gly Lys Val Phe Tyr Asp Lys Asp Ile Asp  
                               40                              45                              50

gct gta atc tat cct gcc agc atg acg aaa atc gca act gcc ctc ttt 307  
 Ala Val Ile Tyr Pro Ala Ser Met Thr Lys Ile Ala Thr Ala Leu Phe  
                               55                              60                              65

atc cta aag cac tat ccc aca gtc ctc gat act ctc atc aaa gtc aaa 355  
 Ile Leu Lys His Tyr Pro Thr Val Leu Asp Thr Leu Ile Lys Val Lys  
       70                              75                              80                              85

60



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	tat	cgt	agt	cct	ccc	cac	tgg	tta	gaa	act	gat	gga	tct	aca	ata	cag	451
	Tyr	Arg	Ser	Pro	Pro	His	Trp	Leu	Glu	Thr	Asp	Gly	Ser	Thr	Ile	Gln	
				105					110					115			
10	ctc	cat	ctt	cga	gaa	gag	ctt	tta	ggg	tgg	gac	ctg	ttc	cac	gcc	tta	499
	Leu	His	Leu	Arg	Glu	Glu	Leu	Leu	Gly	Trp	Asp	Leu	Phe	His	Ala	Leu	
			120					125					130				
	ctg	gtc	tgt	tct	gct	aat	gat	gct	gcg	aat	gtc	tta	gct	atg	gca	tgt	547
	Leu	Val	Cys	Ser	Ala	Asn	Asp	Ala	Ala	Asn	Val	Leu	Ala	Met	Ala	Cys	
		135					140					145					
20	tgc	gga	tct	gta	gag	aag	ttt	atg	gat	aag	ctg	aac	ttc	ttc	tta	aaa	595
	Cys	Gly	Ser	Val	Glu	Lys	Phe	Met	Asp	Lys	Leu	Asn	Phe	Phe	Leu	Lys	
	150					155					160					165	
	gaa	gaa	atc	ggc	tgc	act	cat	acc	cat	ttt	aat	aat	ccc	cat	ggg	tta	643
	Glu	Glu	Ile	Gly	Cys	Thr	His	Thr	His	Phe	Asn	Asn	Pro	His	Gly	Leu	
					170					175					180		
	cat	cat	ccg	aat	cac	tat	act	aca	acc	cgt	gat	ctt	att	agc	atc	atg	691
	His	His	Pro	Asn	His	Tyr	Thr	Thr	Thr	Arg	Asp	Leu	Ile	Ser	Ile	Met	
				185					190					195			
30	cgt	tgc	gct	ctg	aaa	gaa	cct	cca	ttt	cga	ggg	gtc	atc	tcc	acg	aca	739
	Arg	Cys	Ala	Leu	Lys	Glu	Pro	Pro	Phe	Arg	Gly	Val	Ile	Ser	Thr	Thr	
			200					205					210				
	agc	tat	aaa	ata	ggg	gct	aca	aac	ctg	cat	ggc	gaa	cgg	atc	cta	tcc	787
	Ser	Tyr	Lys	Ile	Gly	Ala	Thr	Asn	Leu	His	Gly	Glu	Arg	Ile	Leu	Ser	
		215					220					225					
40	cca	aca	aac	aaa	ttg	ctt	ctt	cct	ggg	tct	acc	tac	cac	tat	ccc	cca	835
	Pro	Thr	Asn	Lys	Leu	Leu	Leu	Pro	Gly	Ser	Thr	Tyr	His	Tyr	Pro	Pro	
	230				235						240					245	
	gct	tta	gga	ggg	aaa	aca	ggg	acc	acc	aag	act	gca	ggg	aaa	aat	cta	883
	Ala	Leu	Gly	Gly	Lys	Thr	Gly	Thr	Thr	Lys	Thr	Ala	Gly	Lys	Asn	Leu	
					250					255					260		
	att	atg	gct	gct	gaa	aaa	aat	aac	cgc	ctc	ttg	gta	acg	atc	gca	acg	931
	Ile	Met	Ala	Ala	Glu	Lys	Asn	Asn	Arg	Leu	Leu	Val	Thr	Ile	Ala	Thr	
				265					270					275			
50	ggc	tat	tcg	ggt	cct	gtg	agt	gat	ctc	tac	caa	gat	gtc	att	gct	cta	979
	Gly	Tyr	Ser	Gly	Pro	Val	Ser	Asp	Leu	Tyr	Gln	Asp	Val	Ile	Ala	Leu	
			280					285					290				
	tgt	gaa	acg	gta	ttt	aac	gag	ccg	cta	tta	aga	aaa	gag	ctc	gtc	ccc	1027
	Cys	Glu	Thr	Val	Phe	Asn	Glu	Pro	Leu	Leu	Arg	Lys	Glu	Leu	Val	Pro	
		295					300					305					
60	ccc	tcc	gac	tgt	ctc	caa	tta	gaa	ata	gcg	aat	ctt	ggg	aag	ctt	tct	1075
	Pro	Ser	Asp	Cys	Leu	Gln	Leu	Glu	Ile	Ala	Asn	Leu	Gly	Lys	Leu	Ser	
	310					315					320					325	

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tgc cct ctt cct gag gga ctc tac tat gac ttc tat gcc tcc gaa gat 1123  
 Cys Pro Leu Pro Glu Gly Leu Tyr Tyr Asp Phe Tyr Ala Ser Glu Asp  
 330 335 340

cgc gaa cct ctt tct gta tct ttt att gca cat gcg gac gcc ttc cct 1171  
 Arg Glu Pro Leu Ser Val Ser Phe Ile Ala His Ala Asp Ala Phe Pro  
 345 350 355

10 att gaa caa gga gat ctt ctt ggt cat tgg gtt ttt tat gac gat gaa 1219  
 Ile Glu Gln Gly Asp Leu Leu Gly His Trp Val Phe Tyr Asp Asp Glu  
 360 365 370

ggc aag aaa att tct tcc cag cct ttc tat gcc cct tgt cgt ttt gag 1267  
 Gly Lys Lys Ile Ser Ser Gln Pro Phe Tyr Ala Pro Cys Arg Phe Glu  
 375 380 385

20 cgc act atc aag cct tgg aaa ctc tat atg aaa cgt gtc ttc aca tcg 1315  
 Arg Thr Ile Lys Pro Trp Lys Leu Tyr Met Lys Arg Val Phe Thr Ser  
 390 395 400 405

tat aga acc tat atg tct ata acc atg ctg ctc atg tat ttt cgc atc 1363  
 Tyr Arg Thr Tyr Met Ser Ile Thr Met Leu Leu Met Tyr Phe Arg Ile  
 410 415 420

cgc aag cac cgc aag tat aaa aat tta aaa cac tat tct aaa atc 1408  
 Arg Lys His Arg Lys Tyr Lys Asn Leu Lys His Tyr Ser Lys Ile  
 425 430 435

30 taacttttttc ttttaattta taaaaaacca aagggtttatg taagatttgc gcttttcaat 1468  
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 <212> PRT  
 <213> Chlamydia pneumoniae

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 <222> (156)..(164)

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50 <210> 13  
 <211> 2100  
 <212> DNA  
 <213> Chlamydia pneumoniae

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 <222> (101)..(2035)

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60

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	Met Ala Ser Asn Pro	
	1 5	
	att tta cag ata gag gat cta tcc ata acc ttg gca aaa caa cgc caa	163
	Ile Leu Gln Ile Glu Asp Leu Ser Ile Thr Leu Ala Lys Gln Arg Gln	
	10 10 15 20	
10	cag tac ccc atc gtc caa tct tta tcg ttt act atc aat gaa gga caa	211
	Gln Tyr Pro Ile Val Gln Ser Leu Ser Phe Thr Ile Asn Glu Gly Gln	
	25 30 35	
	acc tta gca atc att gga gaa tca gga tca gga aaa tct gtc tct gcg	259
	Thr Leu Ala Ile Ile Gly Glu Ser Gly Ser Gly Lys Ser Val Ser Ala	
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	His Ala Ile Leu Arg Leu Leu Pro Cys Pro Pro Phe Ser Val Ser Gly	
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	Gln Val Asn Phe Gln Gly His Asn Leu Leu Thr Ala Ser Arg Ser Ile	
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	caa aaa aag att ata ggg aca gaa att tct atg atc ttt caa aac ccg	403
	Gln Lys Lys Ile Ile Gly Thr Glu Ile Ser Met Ile Phe Gln Asn Pro	
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	Gln Ala Ser Leu Asn Pro Val Phe Thr Ile Glu Gln Gln Phe Arg Glu	
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	Ile Ile His Thr His Leu Ala Leu Thr Ala Glu Val Ala Lys Glu Lys	
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	Met Leu Tyr Ala Leu Glu Glu Thr Gly Phe His Asp Pro Arg Leu Cys	
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	Leu Asn Leu Tyr Pro His Gln Leu Ser Gly Gly Met Leu Gln Arg Ile	
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	Cys Ile Ala Met Ala Leu Leu Cys Ser Pro Lys Leu Leu Ile Ala Asp	
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	Glu Pro Thr Thr Ala Leu Asp Val Ser Val Gln Tyr Gln Ile Leu Gln	
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	Leu Leu Lys Thr Leu Gln Lys Lys Thr Gly Met Ser Leu Leu Ile Ile	
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	Thr His Asn Met Gly Val Ala Glu Thr Ala Asp Asp Val Leu Val	
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	His	Asn	Pro	Ser	His	Pro	Tyr	Thr	Arg	Asp	Leu	Leu	Ala	Ser	Arg	Pro	
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	Ser	Leu	Gln	Pro	Gln	Gln	Leu	Gly	Ser	Phe	Asn	Pro	Ile	Pro	Gly	Gln	
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	Cys	Ser	Lys	Ile	Leu	Asn	Arg	Cys	Ser	Ala	Glu	Ala	Pro	Glu	Ile	Tyr	
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	Pro	Val	Arg	Glu	Gly	His	Lys	Val	Arg	Val	Gly	Cys	Met	Thr	Thr	Asn	
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	Phe	Pro	Gln	Pro	Leu	Ile	Gln	Ala	Thr	Ser	Leu	Thr	Lys	His	Tyr	Tyr	
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	Gly	Glu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Ala	Leu	Ala	Leu	Ala	Gly	
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	Lys	Leu	His	Ser	Lys	His	Gly	Arg	His	Gln	Leu	Arg	Ser	Gln	Val	Arg	
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	Leu	Val	Phe	Gln	Asn	Pro	Gln	Ala	Ser	Leu	Asn	Pro	Arg	Lys	Thr	Ile	
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	Leu	Asp	Ser	Leu	Gly	His	Ser	Leu	Leu	Tyr	His	Lys	Leu	Val	Pro	Lys	
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	Glu	Lys	Val	Leu	Ala	Thr	Val	Arg	Glu	Tyr	Leu	Glu	Leu	Val	Gly	Leu	
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10 att att tgt gac gaa att gtt tct gct cta gat tta tct att caa gca 1651
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caa att ctg aat atg ctt gcc gag ctg caa aaa aaa ctc agc ctc aca 1699
Gln Ile Leu Asn Met Leu Ala Glu Leu Gln Lys Lys Leu Ser Leu Thr
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20 tat ctc ttc att tcg cat gat ctt gcc gtt gta cgc tcg ttc tgc aca 1747
Tyr Leu Phe Ile Ser His Asp Leu Ala Val Val Arg Ser Phe Cys Thr
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Glu Val Phe Ile Met Tyr Lys Gly Gln Ile Val Glu Lys Gly Asn Thr
550 555 560 565

aaa cgc att ttt tct gat cca caa cat cct tat acg cgc atg ttg tta 1843
Lys Arg Ile Phe Ser Asp Pro Gln His Pro Tyr Thr Arg Met Leu Leu
570 575 580

30 aat gcc caa ctt cca gag act cct gat caa agg caa tct aaa cct ata 1891
Asn Ala Gln Leu Pro Glu Thr Pro Asp Gln Arg Gln Ser Lys Pro Ile
585 590 595

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Phe Gln Glu Tyr His Lys Asp Ser Glu Glu Ser Cys Ser Thr Gly Cys
600 605 610

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&lt;222&gt; (101)..(2194)

&lt;400&gt; 15

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30 aaa gtt aaa gag cga ttg aca aag cgg gaa ctt acc tgt gaa gac ctt 211  
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 Lys Asp Asn Gly Tyr Thr Val Asn Phe Glu Asp Ile Ser Ile Leu Glu  
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 70 75 80 85

tct gta gat gat tta tct aca atc tta cta caa gtc tta aaa atg cat 403  
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 Pro His Leu Ser Lys Leu Ser Thr Val Val Thr Asp Ser Ser Leu Lys  
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gaa acg tgt gaa gct gtt gtg gtt acc cga gtg ttc cgt ctt tac agg 547  
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	Asp	Ala	Ile	Val	Ser	Ala	Ser	Glu	Ala	Thr	Arg	His	Val	Ile	Ile	Ser	
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	Ala	Asn	Pro	Ala	Ala	Leu	Val	Ser	Tyr	Cys	Gln	Asp	Val	Leu	Gly	Thr	
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	Lys	Ile	Phe	Val	Val	Ser	Ser	Pro	Arg	Leu	Ala	Asn	Lys	Ala	Glu	Gln	
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	Leu	Leu	Lys	Ser	Leu	Asp	Val	Pro	Glu	Met	Ala	His	Thr	Leu	Asp	Asp	
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	Pro	Ala	Ser	Thr	Ala	Leu	Ala	Leu	Gly	Gly	Thr	Gly	Thr	Thr	Ser	Pro	
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	Asp Phe Gly Val Gln Trp Val Ala Leu Gly Asp Glu Gln Ser Lys Val	
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	Gly Asp Thr Val Ile Val Leu Asn Pro Arg Ile Met Ala Gln Asp Thr	
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	Gln Gln Ala Ser Phe Phe Val Gly Gln Thr Val Pro Tyr Gln Thr Ile	
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	aaa tac tat atc caa gaa aca gga act gta acg caa aat atc gat tat	1699
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	Arg Asp Lys Thr Thr Lys Val Val Ser Gly Val Pro Leu Leu Asn Ser	
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 650 655 660

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gaa gct gat gaa gga tcc atg caa gtg gcc cct cgc cat gct cct gaa 2131  
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 665 670 675

tgc caa gga cct cct tct tta cag gct gaa agt gac ttt aaa ata ata 2179  
 Cys Gln Gly Pro Pro Ser Leu Gln Ala Glu Ser Asp Phe Lys Ile Ile  
 680 685 690

20

gaa ata gaa gct cag tagtggtata taaaagagga agatgatatt ctccgccgtg 2234  
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 Met Ser Arg Lys Asp  
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	ctt	cac	tgt	gga	aat	aag	ttt	ttc	ggg	gtg	gga	tta	gct	ccc	gta	gtt	595
	Leu	His	Cys	Gly	Asn	Lys	Phe	Phe	Gly	Val	Gly	Leu	Ala	Pro	Val	Val	
	150					155				160						165	
40	gta	aat	atc	att	tgg	att	ttc	ttt	gtt	ata	gcg	gct	cgt	cat	tca	gat	643
	Val	Asn	Ile	Ile	Trp	Ile	Phe	Phe	Val	Ile	Ala	Ala	Arg	His	Ser	Asp	
					170					175					180		
	cct	aga	gag	cgt	att	atc	ggg	tta	tcc	gtg	gct	cta	gtt	atc	ggg	ttt	691
	Pro	Arg	Glu	Arg	Ile	Ile	Gly	Leu	Ser	Val	Ala	Leu	Val	Ile	Gly	Phe	
				185					190					195			
50	ttc	ttc	gaa	tgg	tta	atc	acg	gtt	cct	gga	gta	tgg	aaa	ttt	cta	tta	739
	Phe	Phe	Glu	Trp	Leu	Ile	Thr	Val	Pro	Gly	Val	Trp	Lys	Phe	Leu	Leu	
			200					205					210				
	gaa	gcg	aag	agc	cca	cct	caa	gaa	cac	gat	agt	gtt	cga	gct	tta	tta	787
	Glu	Ala	Lys	Ser	Pro	Pro	Gln	Glu	His	Asp	Ser	Val	Arg	Ala	Leu	Leu	
		215					220					225					
	gct	ccc	tta	tct	ttg	ggg	att	tta	act	tca	agc	atc	ttc	cag	ctg	aac	835
	Ala	Pro	Leu	Ser	Leu	Gly	Ile	Leu	Thr	Ser	Ser	Ile	Phe	Gln	Leu	Asn	
	230					235				240						245	
60	ctt	ctt	tct	gat	atc	tgc	ttg	gct	cgc	tat	gta	cat	gaa	ata	ggc	cct	883
	Leu	Leu	Ser	Asp	Ile	Cys	Leu	Ala	Arg	Tyr	Val	His	Glu	Ile	Gly	Pro	
					250					255					260		

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	cta	tat	ctt	atg	tac	tcc	tta	aag	att	tat	cag	ctc	ccc	ata	cat	ctc	931
	Leu	Tyr	Leu	Met	Tyr	Ser	Leu	Lys	Ile	Tyr	Gln	Leu	Pro	Ile	His	Leu	
				265					270					275			
	ttt	ggc	ttt	ggg	gtg	ttt	acc	gtt	ctc	ctc	cca	gca	att	tct	cgt	tgt	979
	Phe	Gly	Phe	Gly	Val	Phe	Thr	Val	Leu	Leu	Pro	Ala	Ile	Ser	Arg	Cys	
			280					285					290				
10	gta	cag	cga	gaa	gat	cat	gag	agg	gga	ttg	aaa	ctt	atg	aag	ttc	gtt	1027
	Val	Gln	Arg	Glu	Asp	His	Glu	Arg	Gly	Leu	Lys	Leu	Met	Lys	Phe	Val	
		295					300					305					
	ctc	acc	cta	acc	atg	tcc	gta	atg	atc	att	atg	aca	gca	ggg	cta	ttg	1075
	Leu	Thr	Leu	Thr	Met	Ser	Val	Met	Ile	Ile	Met	Thr	Ala	Gly	Leu	Leu	
	310					315					320					325	
20	ctc	tta	gct	tta	cct	gga	gtc	cgt	gtc	ctt	tat	gaa	cac	gga	ctt	ttc	1123
	Leu	Leu	Ala	Leu	Pro	Gly	Val	Arg	Val	Leu	Tyr	Glu	His	Gly	Leu	Phe	
					330					335					340		
	cct	cag	agt	gct	gtc	tac	gct	att	gtt	cgt	gta	ttg	cga	ggg	tat	ggg	1171
	Pro	Gln	Ser	Ala	Val	Tyr	Ala	Ile	Val	Arg	Val	Leu	Arg	Gly	Tyr	Gly	
				345					350					355			
	gcc	agt	att	atc	cct	atg	gcc	ttg	gct	cct	tta	gtc	tct	gtt	ctt	ttt	1219
	Ala	Ser	Ile	Ile	Pro	Met	Ala	Leu	Ala	Pro	Leu	Val	Ser	Val	Leu	Phe	
			360					365					370				
30	tat	gca	cag	cgg	cag	tat	gct	gtt	ccg	ctc	ttt	ata	gga	atc	ggg	acg	1267
	Tyr	Ala	Gln	Arg	Gln	Tyr	Ala	Val	Pro	Leu	Phe	Ile	Gly	Ile	Gly	Thr	
		375					380					385					
	gct	ttg	gcc	aat	att	gtt	tta	agc	ttg	gtt	cta	ggg	cgt	tgg	gtt	tta	1315
	Ala	Leu	Ala	Asn	Ile	Val	Leu	Ser	Leu	Val	Leu	Gly	Arg	Trp	Val	Leu	
	390					395					400					405	
40	aaa	gac	gtc	tcg	ggc	att	tcc	tat	gct	aca	tcc	ata	act	gct	tgg	gtg	1363
	Lys	Asp	Val	Ser	Gly	Ile	Ser	Tyr	Ala	Thr	Ser	Ile	Thr	Ala	Trp	Val	
					410					415					420		
	cag	tta	tat	ttc	ctc	tgg	tat	tat	tct	tcg	aaa	aga	ctc	cct	atg	tac	1411
	Gln	Leu	Tyr	Phe	Leu	Trp	Tyr	Tyr	Ser	Ser	Lys	Arg	Leu	Pro	Met	Tyr	
				425					430					435			
	tct	aag	tta	ctt	tgg	gag	agc	atc	cgg	cgt	tcc	ata	aaa	gtt	atg	gga	1459
	Ser	Lys	Leu	Leu	Trp	Glu	Ser	Ile	Arg	Arg	Ser	Ile	Lys	Val	Met	Gly	
			440				445						450				
50	acc	act	atg	ctt	gct	tgt	atg	att	act	cta	ggc	tta	aat	atc	ctt	acg	1507
	Thr	Thr	Met	Leu	Ala	Cys	Met	Ile	Thr	Leu	Gly	Leu	Asn	Ile	Leu	Thr	
			455				460					465					
	caa	act	aca	tat	gta	att	ttc	tta	aac	ccc	ctc	aca	cca	ctt	gct	tgg	1555
	Gln	Thr	Thr	Tyr	Val	Ile	Phe	Leu	Asn	Pro	Leu	Thr	Pro	Leu	Ala	Trp	
	470					475					480					485	
60	ccc	tta	tcc	tcc	ata	acg	gct	caa	gca	att	gct	ttt	tta	tct	gag	agc	1603
	Pro	Leu	Ser	Ser	Ile	Thr	Ala	Gln	Ala	Ile	Ala	Phe	Leu	Ser	Glu	Ser	
					490					495					500		

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tgc att ttc ttg gct ttt ttg ttt ggt ttt gca aaa ctg ctt cga gta 1651  
 Cys Ile Phe Leu Ala Phe Leu Phe Gly Phe Ala Lys Leu Leu Arg Val  
                   505                                  510                                  515

gaa gat ctt att aat ttg gct tct ttt gaa tac tgg cgt ggg caa cgg 1699  
 Glu Asp Leu Ile Asn Leu Ala Ser Phe Glu Tyr Trp Arg Gly Gln Arg  
                   520                                  525                                  530

10

ggt ctt ttg caa aga caa cac gtg atg caa gac act caa aat 1741  
 Gly Leu Leu Gln Arg Gln His Val Met Gln Asp Thr Gln Asn  
                   535                                  540                                  545

taatcatggt tggtttcttgt agctcagtcg ctttctttta gctttaagtt ttgatagcct 1801  
 gcttggtctt ctgtttctac acttaatat gatactaagg atactatgaa aaaacaggta 1861  
 tatcaatggt tagcgagtgt gggtctttta gcgctgaca 1900

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30

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           1                                  5

<210> 19  
 <211> 3150  
 <212> DNA  
 <213> Chlamydia pneumoniae

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<220>  
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aataccttaa agctgagagt cattgcacat ttaaccaca atg aaa aca tca agg 115  
                                                           Met Lys Thr Ser Arg  
                                                                   1                                  5

50

aat aaa cag tgc aaa ata aca gat ccc tta agt aaa tct tcc ttc ttt 163  
 Asn Lys Gln Cys Lys Ile Thr Asp Pro Leu Ser Lys Ser Ser Phe Phe  
                                   10                                  15                                  20

gtt gga gcc tta att tta ggt aaa act aca ata ctc ctt aat gcg act 211  
 Val Gly Ala Leu Ile Leu Gly Lys Thr Thr Ile Leu Leu Asn Ala Thr  
                   25                                  30                                  35

ccg ttg tct gac tat ttt gat aat caa gca aat caa ctc aca aca ctc 259  
 Pro Leu Ser Asp Tyr Phe Asp Asn Gln Ala Asn Gln Leu Thr Thr Leu  
                   40                                  45                                  50

60

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	ttc	cct	cta	att	gat	act	ctt	act	aac	atg	act	ccc	tac	tct	cat	aga	307
	Phe	Pro	Leu	Ile	Asp	Thr	Leu	Thr	Asn	Met	Thr	Pro	Tyr	Ser	His	Arg	
	55						60					65					
	gca	aca	ctt	ttt	gga	gtt	agg	gat	gac	act	aac	caa	gac	att	gtc	ctc	355
	Ala	Thr	Leu	Phe	Gly	Val	Arg	Asp	Asp	Thr	Asn	Gln	Asp	Ile	Val	Leu	
	70					75					80					85	
10	gat	cac	cag	aat	tcc	ata	gaa	agc	tgg	ttc	gaa	aac	ttc	tct	caa	gac	403
	Asp	His	Gln	Asn	Ser	Ile	Glu	Ser	Trp	Phe	Glu	Asn	Phe	Ser	Gln	Asp	
					90					95					100		
	ggc	ggt	gct	ctc	tct	tgc	aaa	tca	ctt	gcc	ata	acg	aat	aca	aaa	aac	451
	Gly	Gly	Ala	Leu	Ser	Cys	Lys	Ser	Leu	Ala	Ile	Thr	Asn	Thr	Lys	Asn	
				105					110					115			
20	caa	att	ctt	ttc	cta	aat	agc	ttt	gct	att	aaa	aga	gct	ggt	gcg	atg	499
	Gln	Ile	Leu	Phe	Leu	Asn	Ser	Phe	Ala	Ile	Lys	Arg	Ala	Gly	Ala	Met	
			120					125					130				
	tat	gtt	gat	ggt	aat	ttc	gat	ctt	tct	gag	aat	cat	ggt	tcc	atc	att	547
	Tyr	Val	Asp	Gly	Asn	Phe	Asp	Leu	Ser	Glu	Asn	His	Gly	Ser	Ile	Ile	
		135					140					145					
	ttc	tct	ggg	aat	tta	agc	ttt	cct	aat	gca	agt	aat	ttc	gct	gat	act	595
	Phe	Ser	Gly	Asn	Leu	Ser	Phe	Pro	Asn	Ala	Ser	Asn	Phe	Ala	Asp	Thr	
	150					155					160					165	
30	tgt	aca	ggg	gga	gct	gtt	tta	tgt	tcg	aaa	aat	ggt	aca	atc	tca	aaa	643
	Cys	Thr	Gly	Gly	Ala	Val	Leu	Cys	Ser	Lys	Asn	Val	Thr	Ile	Ser	Lys	
					170					175					180		
	aat	caa	gga	acc	gca	tac	ttc	att	aac	aac	aag	gca	aaa	tct	tca	gga	691
	Asn	Gln	Gly	Thr	Ala	Tyr	Phe	Ile	Asn	Asn	Lys	Ala	Lys	Ser	Ser	Gly	
				185					190					195			
40	gga	gca	atc	caa	gct	gca	atc	ata	aac	att	aag	gac	aac	act	ggc	cct	739
	Gly	Ala	Ile	Gln	Ala	Ala	Ile	Ile	Asn	Ile	Lys	Asp	Asn	Thr	Gly	Pro	
			200					205					210				
	tgc	ctg	ttt	ttt	aat	aat	gct	gca	ggc	gga	aca	gcg	ggg	ggc	gcg	ttg	787
	Cys	Leu	Phe	Phe	Asn	Asn	Ala	Ala	Gly	Gly	Thr	Ala	Gly	Gly	Ala	Leu	
		215					220					225					
	ttc	gct	aat	gct	tgt	aga	att	gag	aat	aat	tct	cag	cct	atc	tat	ttt	835
	Phe	Ala	Asn	Ala	Cys	Arg	Ile	Glu	Asn	Asn	Ser	Gln	Pro	Ile	Tyr	Phe	
	230					235					240					245	
50	ttg	aat	aac	caa	tca	ggt	ctg	ggt	ggt	gca	ata	aga	gta	cat	caa	gag	883
	Leu	Asn	Asn	Gln	Ser	Gly	Leu	Gly	Gly	Ala	Ile	Arg	Val	His	Gln	Glu	
					250					255					260		
	tgc	att	ctt	aca	aag	aat	acc	ggt	tct	gtg	atc	ttc	aac	aat	aat	ttt	931
	Cys	Ile	Leu	Thr	Lys	Asn	Thr	Gly	Ser	Val	Ile	Phe	Asn	Asn	Asn	Phe	
				265				270						275			
60	gcc	atg	gaa	gcg	gac	atc	tct	gct	aac	cat	tcc	tct	gga	ggg	gct	atc	979
	Ala	Met	Glu	Ala	Asp	Ile	Ser	Ala	Asn	His	Ser	Ser	Gly	Gly	Ala	Ile	
			280					285					290				

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	tat tgc att agt tgt tct ata aaa gac aac cca gga att gca gcc ttc	1027
	Tyr Cys Ile Ser Cys Ser Ile Lys Asp Asn Pro Gly Ile Ala Ala Phe	
	295 300 305	
	gat aat aat act gca gca cga gat gga ggt gct atc tgt aca caa tct	1075
	Asp Asn Asn Thr Ala Ala Arg Asp Gly Gly Ala Ile Cys Thr Gln Ser	
	310 315 320 325	
10	cta act ata caa gac agt ggt ccc gtc tat ttc aca aac aat cag gga	1123
	Leu Thr Ile Gln Asp Ser Gly Pro Val Tyr Phe Thr Asn Asn Gln Gly	
	330 335 340	
	act tgg ggc ggc gct atc atg ctc cgt caa gat ggt gca tgc act tta	1171
	Thr Trp Gly Gly Ala Ile Met Leu Arg Gln Asp Gly Ala Cys Thr Leu	
	345 350 355	
20	ttt gct gat cag gga gat att att ttt tat aat aat aga cac ttc aaa	1219
	Phe Ala Asp Gln Gly Asp Ile Ile Phe Tyr Asn Asn Arg His Phe Lys	
	360 365 370	
	gat act ttc agc aat cat gtt tct gta aac tgc acg cgt aat gtc tca	1267
	Asp Thr Phe Ser Asn His Val Ser Val Asn Cys Thr Arg Asn Val Ser	
	375 380 385	
	tta aca gtt gga gca agt caa ggt cat tct gct acc ttc tat gat ccc	1315
	Leu Thr Val Gly Ala Ser Gln Gly His Ser Ala Thr Phe Tyr Asp Pro	
	390 395 400 405	
30	ata cta caa aga tat act ata caa aac tct atc caa aaa ttt aat cct	1363
	Ile Leu Gln Arg Tyr Thr Ile Gln Asn Ser Ile Gln Lys Phe Asn Pro	
	410 415 420	
	aat cca gaa cac ctc gga act atc ttg ttc tcc tca aca tat att ccg	1411
	Asn Pro Glu His Leu Gly Thr Ile Leu Phe Ser Ser Thr Tyr Ile Pro	
	425 430 435	
40	gat aca tcg act tct cgt gat gac ttc att tca cat ttc aga aac cac	1459
	Asp Thr Ser Thr Ser Arg Asp Asp Phe Ile Ser His Phe Arg Asn His	
	440 445 450	
	att gga ctg tac aac ggc aca ctc gct ctt gaa gat cga gca gag tgg	1507
	Ile Gly Leu Tyr Asn Gly Thr Leu Ala Leu Glu Asp Arg Ala Glu Trp	
	455 460 465	
	aaa gtc tat aaa ttt gat caa ttt ggt ggg act cta cgg tta ggc agt	1555
	Lys Val Tyr Lys Phe Asp Gln Phe Gly Gly Thr Leu Arg Leu Gly Ser	
	470 475 480 485	
50	aga gct gtg ttt tct aca aca gac gaa gaa caa agt agc agt agt gtg	1603
	Arg Ala Val Phe Ser Thr Thr Asp Glu Glu Gln Ser Ser Ser Ser Val	
	490 495 500	
	ggt tct gta att aac atc aat aat ctt gca att aac ctt ccc tct atc	1651
	Gly Ser Val Ile Asn Ile Asn Asn Leu Ala Ile Asn Leu Pro Ser Ile	
	505 510 515	
60	tta ggc aac aga gtt gct ccc aag cta tgg att cgc ccc aca ggt tca	1699
	Leu Gly Asn Arg Val Ala Pro Lys Leu Trp Ile Arg Pro Thr Gly Ser	
	520 525 530	

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	tca	gca	ccc	tat	agc	gaa	gat	aat	aac	cct	ata	atc	aat	ctc	tca	gga	1747
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		535					540					545					
	cct	ttg	agc	cta	ctg	gat	gac	gag	aac	cta	gat	ccc	tat	gat	act	gca	1795
	Pro	Leu	Ser	Leu	Leu	Asp	Asp	Glu	Asn	Leu	Asp	Pro	Tyr	Asp	Thr	Ala	
	550					555					560					565	
10	gac	ctt	gcc	caa	cct	atc	gca	gaa	gtt	cct	ctt	ctg	tat	ctc	tta	gac	1843
	Asp	Leu	Ala	Gln	Pro	Ile	Ala	Glu	Val	Pro	Leu	Leu	Tyr	Leu	Leu	Asp	
					570					575					580		
	gtc	aca	gct	aaa	cat	att	aat	acg	gat	aat	ttc	tac	cct	gag	ggc	cta	1891
	Val	Thr	Ala	Lys	His	Ile	Asn	Thr	Asp	Asn	Phe	Tyr	Pro	Glu	Gly	Leu	
				585					590					595			
20	aat	aca	act	caa	cac	tac	ggc	tac	caa	ggc	gtt	tgg	tcc	cct	tac	tgg	1939
	Asn	Thr	Thr	Gln	His	Tyr	Gly	Tyr	Gln	Gly	Val	Trp	Ser	Pro	Tyr	Trp	
			600					605					610				
	atc	gaa	aca	atc	aca	act	tct	gat	acc	tct	tct	gaa	gat	act	gtg	aat	1987
	Ile	Glu	Thr	Ile	Thr	Thr	Ser	Asp	Thr	Ser	Ser	Glu	Asp	Thr	Val	Asn	
		615						620				625					
	act	tta	cat	cgc	cag	ctt	tat	ggc	gat	tgg	aca	cct	aca	gga	tat	aag	2035
	Thr	Leu	His	Arg	Gln	Leu	Tyr	Gly	Asp	Trp	Thr	Pro	Thr	Gly	Tyr	Lys	
	630					635					640					645	
30	gta	aac	cca	gaa	aac	aaa	gga	gac	att	gcc	cta	tct	gcc	ttc	tgg	caa	2083
	Val	Asn	Pro	Glu	Asn	Lys	Gly	Asp	Ile	Ala	Leu	Ser	Ala	Phe	Trp	Gln	
					650					655					660		
	tct	ttc	cat	aac	tta	ttt	gcg	aca	cta	cgt	tat	caa	aca	cag	caa	ggc	2131
	Ser	Phe	His	Asn	Leu	Phe	Ala	Thr	Leu	Arg	Tyr	Gln	Thr	Gln	Gln	Gly	
				665					670					675			
40	caa	ata	gca	cct	aca	gct	tct	gga	gaa	gct	act	cga	ctc	ttc	gtg	cat	2179
	Gln	Ile	Ala	Pro	Thr	Ala	Ser	Gly	Glu	Ala	Thr	Arg	Leu	Phe	Val	His	
			680					685					690				
	caa	aat	agc	aac	aat	gat	gcg	aaa	gga	ttc	cat	atg	gaa	gct	acg	ggc	2227
	Gln	Asn	Ser	Asn	Asn	Asp	Ala	Lys	Gly	Phe	His	Met	Glu	Ala	Thr	Gly	
		695					700					705					
	tat	tct	ttg	gga	aca	acc	tca	aac	act	gct	tct	aat	cat	agc	ttt	ggc	2275
	Tyr	Ser	Leu	Gly	Thr	Thr	Ser	Asn	Thr	Ala	Ser	Asn	His	Ser	Phe	Gly	
	710					715					720					725	
50	gta	aac	ttc	tcc	caa	ctt	ttc	agt	aat	ctc	tac	gag	agc	cac	tcc	gac	2323
	Val	Asn	Phe	Ser	Gln	Leu	Phe	Ser	Asn	Leu	Tyr	Glu	Ser	His	Ser	Asp	
					730					735						740	
	aat	tcc	gtg	gct	tcg	cat	acg	aca	act	gta	gcg	ctc	cag	atc	aat	aat	2371
	Asn	Ser	Val	Ala	Ser	His	Thr	Thr	Thr	Val	Ala	Leu	Gln	Ile	Asn	Asn	
				745					750					755			
60	cct	tgg	ctg	caa	gag	aga	ttc	tct	aca	tct	gca	tct	cta	gcc	tac	agc	2419
	Pro	Trp	Leu	Gln	Glu	Arg	Phe	Ser	Thr	Ser	Ala	Ser	Leu	Ala	Tyr	Ser	
			760					765					770				

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tac agc aac cac cat atc aaa gca tct gga tat tct gga aaa ata caa 2467  
 Tyr Ser Asn His His Ile Lys Ala Ser Gly Tyr Ser Gly Lys Ile Gln  
 775 780 785

acg gaa ggc aaa tgt tat agt acg aca tta ggg gcg gct ctc tct tgc 2515  
 Thr Glu Gly Lys Cys Tyr Ser Thr Thr Leu Gly Ala Ala Leu Ser Cys  
 790 795 800 805

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 tct cta tct cta caa tgg cga tca cga cct ctc cac ttc act cct ttt 2563  
 Ser Leu Ser Leu Gln Trp Arg Ser Arg Pro Leu His Phe Thr Pro Phe  
 810 815 820

atc caa gca att gcc gtt cgt tct aat caa act gcg ttt caa gaa agt 2611  
 Ile Gln Ala Ile Ala Val Arg Ser Asn Gln Thr Ala Phe Gln Glu Ser  
 825 830 835

20
   
 gga gat aaa gct aga aaa ttt tct gtt cat aaa ccc tta tat aac ctg 2659  
 Gly Asp Lys Ala Arg Lys Phe Ser Val His Lys Pro Leu Tyr Asn Leu  
 840 845 850

aca gtc cct ctg gga att cag agc gct tgg gaa tcc aag ttc cgt ctt 2707  
 Thr Val Pro Leu Gly Ile Gln Ser Ala Trp Glu Ser Lys Phe Arg Leu  
 855 860 865

30
   
 cct acc tat tgg aac ata gag ctt gct tat cag cct gtc ctc tac caa 2755  
 Pro Thr Tyr Trp Asn Ile Glu Leu Ala Tyr Gln Pro Val Leu Tyr Gln  
 870 875 880 885

caa aat cct gag atc aac gtg agt cta gaa tct agt gga tcg tca tgg 2803  
 Gln Asn Pro Glu Ile Asn Val Ser Leu Glu Ser Ser Gly Ser Ser Trp  
 890 895 900

ctc cta tca gga acc acc ctt gct cgc aat gcc att gct ttt aaa gga 2851  
 Leu Leu Ser Gly Thr Thr Leu Ala Arg Asn Ala Ile Ala Phe Lys Gly  
 905 910 915

40
   
 aga aac caa att ttt atc ttc cct aaa ctt tcg gtg ttc tta gac tat 2899  
 Arg Asn Gln Ile Phe Ile Phe Pro Lys Leu Ser Val Phe Leu Asp Tyr  
 920 925 930

caa ggc tcg gta tcc tca tca acg acg aca cat tac ctt cac gca gga 2947  
 Gln Gly Ser Val Ser Ser Ser Thr Thr Thr His Tyr Leu His Ala Gly  
 935 940 945

50
   
 acg acc ttt aag ttt taaaagcatg ttatatagac aatgcaacct gtaaagacca 3002  
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&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Chlamydia pneumoniae

60

&lt;220&gt;



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&lt;221&gt; SITE

&lt;222&gt; (119)..(127)

&lt;400&gt; 20

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5

10

&lt;210&gt; 21

&lt;211&gt; 3200

&lt;212&gt; DNA

&lt;213&gt; Chlamydia pneumoniae

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(3100)

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&lt;400&gt; 21

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 Met Leu Leu Pro Phe  
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	Asn Val Cys Pro Asn Ser Gly Gly Ala Ile Tyr Ala Ala Gln Asn Cys	
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	acg atc tcc aag aat cag aac tat gca ttt act aca aac ttg gtc tct	451
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	Trp Ile Tyr Pro Thr Lys Thr Gly Ser Thr Tyr Thr Glu Asp Ser Asn	
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&lt;211&gt; 9

&lt;212&gt; PRT

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&lt;221&gt; SITE

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&lt;400&gt; 24

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<220>

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 Ala Phe Ala Glu Thr Arg Leu Gly Gly Asn Phe Val Pro Pro Ile Thr  
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 Phe Leu Gly Ala Ser Phe Ser Ser Ser Phe Ile Asn Ser Ser Ser Asn  
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	Ser	Ile	Lys	Phe	Phe	Gly	Asn	Leu	Ala	Asn	Phe	Gly	Ser	Ala	Ile	Ser	
				185					190					195			
	agt	tct	ccc	acg	gca	gtc	gtt	aaa	ttc	atc	aat	aac	acc	gct	acc	atg	738
	Ser	Ser	Pro	Thr	Ala	Val	Val	Lys	Phe	Ile	Asn	Asn	Thr	Ala	Thr	Met	
			200					205					210				
10	agc	ttc	tcc	cat	aac	ttt	act	tcg	tca	gga	ggc	ggc	gtg	att	tat	gga	786
	Ser	Phe	Ser	His	Asn	Phe	Thr	Ser	Ser	Gly	Gly	Gly	Val	Ile	Tyr	Gly	
		215					220					225					
	gga	agc	tct	ctc	ctt	ttt	gaa	aac	aat	tct	gga	tgc	atc	atc	ttc	acc	834
	Gly	Ser	Ser	Leu	Leu	Phe	Glu	Asn	Asn	Ser	Gly	Cys	Ile	Ile	Phe	Thr	
	230					235					240					245	
20	gcc	aac	tcc	tgt	gtg	aac	agc	tta	aaa	ggc	gtc	acc	cct	tca	tca	gga	882
	Ala	Asn	Ser	Cys	Val	Asn	Ser	Leu	Lys	Gly	Val	Thr	Pro	Ser	Ser	Gly	
					250					255					260		
	acc	tat	gct	tta	gga	agt	ggc	gga	gcc	atc	tgc	atc	cct	acg	gga	act	930
	Thr	Tyr	Ala	Leu	Gly	Ser	Gly	Gly	Ala	Ile	Cys	Ile	Pro	Thr	Gly	Thr	
				265					270					275			
	ttc	gaa	tta	aaa	aac	aat	cag	ggg	aag	tgc	acc	ttc	tct	tat	aat	ggc	978
	Phe	Glu	Leu	Lys	Asn	Asn	Gln	Gly	Lys	Cys	Thr	Phe	Ser	Tyr	Asn	Gly	
			280					285					290				
30	aca	cca	aat	gat	gcg	ggt	gcg	atc	tac	gcc	gaa	acc	tgc	aac	atc	gta	1026
	Thr	Pro	Asn	Asp	Ala	Gly	Ala	Ile	Tyr	Ala	Glu	Thr	Cys	Asn	Ile	Val	
		295				300						305					
	ggg	aac	cag	ggt	gcc	ttg	ctc	cta	gat	agc	aac	act	gca	gcg	aga	aat	1074
	Gly	Asn	Gln	Gly	Ala	Leu	Leu	Leu	Asp	Ser	Asn	Thr	Ala	Ala	Arg	Asn	
	310					315					320					325	
40	ggc	gga	gcc	atc	tgt	gct	aaa	gtg	ctc	aat	att	caa	gga	cgc	ggt	cct	1122
	Gly	Gly	Ala	Ile	Cys	Ala	Lys	Val	Leu	Asn	Ile	Gln	Gly	Arg	Gly	Pro	
					330					335					340		
	att	gaa	ttc	tct	aga	aac	cgc	gcg	gag	aag	ggt	gga	gct	att	ttc	ata	1170
	Ile	Glu	Phe	Ser	Arg	Asn	Arg	Ala	Glu	Lys	Gly	Gly	Ala	Ile	Phe	Ile	
				345					350					355			
	ggc	ccc	tct	gtt	gga	gac	cct	gcg	aag	caa	aca	tcg	aca	ctt	acg	att	1218
	Gly	Pro	Ser	Val	Gly	Asp	Pro	Ala	Lys	Gln	Thr	Ser	Thr	Leu	Thr	Ile	
			360					365					370				
50	ttg	gct	tcc	gaa	ggt	gat	att	gcg	ttc	caa	gga	aac	atg	ctc	aat	aca	1266
	Leu	Ala	Ser	Glu	Gly	Asp	Ile	Ala	Phe	Gln	Gly	Asn	Met	Leu	Asn	Thr	
		375					380					385					
	aaa	cct	gga	atc	cgc	aat	gcc	atc	act	gta	gaa	gca	ggg	gga	gag	att	1314
	Lys	Pro	Gly	Ile	Arg	Asn	Ala	Ile	Thr	Val	Glu	Ala	Gly	Gly	Glu	Ile	
	390					395					400					405	
60	gtg	tct	cta	tct	gca	caa	gga	ggc	tca	cgt	ctt	gta	ttt	tat	gat	ccc	1362
	Val	Ser	Leu	Ser	Ala	Gln	Gly	Gly	Ser	Arg	Leu	Val	Phe	Tyr	Asp	Pro	
					410					415					420		



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	att	aca	cat	agc	ctc	cca	acc	aca	agt	ccg	tct	aat	aaa	gac	att	aca	1410
	Ile	Thr	His	Ser	Leu	Pro	Thr	Thr	Ser	Pro	Ser	Asn	Lys	Asp	Ile	Thr	
				425					430					435			
	atc	aac	gct	aat	ggc	gct	tca	gga	tct	gta	gtc	ttt	aca	agt	aag	gga	1458
	Ile	Asn	Ala	Asn	Gly	Ala	Ser	Gly	Ser	Val	Val	Phe	Thr	Ser	Lys	Gly	
			440					445					450				
10	ctc	tcc	tct	aca	gaa	ctc	ctg	ttg	cct	gcc	aac	acg	aca	act	ata	ctt	1506
	Leu	Ser	Ser	Thr	Glu	Leu	Leu	Leu	Pro	Ala	Asn	Thr	Thr	Thr	Ile	Leu	
		455					460					465					
	cta	gga	aca	gtc	aag	atc	gct	agt	gga	gaa	ctg	aag	att	act	gac	aat	1554
	Leu	Gly	Thr	Val	Lys	Ile	Ala	Ser	Gly	Glu	Leu	Lys	Ile	Thr	Asp	Asn	
	470					475					480					485	
	gcg	gtt	gtc	aat	gtt	gct	ggc	ttc	gct	act	cag	ggc	tca	ggg	cag	ctt	1602
20	Ala	Val	Val	Asn	Val	Ala	Gly	Phe	Ala	Thr	Gln	Gly	Ser	Gly	Gln	Leu	
				490					495						500		
	acc	ctg	ggc	tct	gga	gga	acc	tta	ggg	ctg	gca	aca	ccc	acg	gga	gca	1650
	Thr	Leu	Gly	Ser	Gly	Gly	Thr	Leu	Gly	Leu	Ala	Thr	Pro	Thr	Gly	Ala	
				505					510					515			
	cct	gcc	gct	gta	gac	ttt	acg	att	gga	aag	tta	gca	ttc	gat	cct	ttt	1698
	Pro	Ala	Ala	Val	Asp	Phe	Thr	Ile	Gly	Lys	Leu	Ala	Phe	Asp	Pro	Phe	
				520				525					530				
30	tcc	ttc	cta	aaa	aga	gat	ttt	gtt	tca	gca	tca	gta	aat	gca	ggc	aca	1746
	Ser	Phe	Leu	Lys	Arg	Asp	Phe	Val	Ser	Ala	Ser	Val	Asn	Ala	Gly	Thr	
		535					540					545					
	aaa	aac	gtc	act	tta	aca	gga	gct	ctg	gtt	ctt	gat	gaa	cat	gac	gtt	1794
	Lys	Asn	Val	Thr	Leu	Thr	Gly	Ala	Leu	Val	Leu	Asp	Glu	His	Asp	Val	
	550					555					560					565	
	aca	gat	ctt	tat	gat	atg	gtg	tca	tta	caa	tct	cca	gta	gca	att	cct	1842
40	Thr	Asp	Leu	Tyr	Asp	Met	Val	Ser	Leu	Gln	Ser	Pro	Val	Ala	Ile	Pro	
					570					575					580		
	atc	gct	gtt	ttc	aaa	gga	gca	acc	gtt	act	aag	aca	gga	ttt	cct	gat	1890
	Ile	Ala	Val	Phe	Lys	Gly	Ala	Thr	Val	Thr	Lys	Thr	Gly	Phe	Pro	Asp	
				585					590					595			
	ggg	gag	att	gcg	act	cca	agc	cac	tac	ggc	tac	caa	gga	aag	tggt	tcc	1938
	Gly	Glu	Ile	Ala	Thr	Pro	Ser	His	Tyr	Gly	Tyr	Gln	Gly	Lys	Trp	Ser	
			600					605					610				
50	tac	aca	tggt	tcc	cgt	ccc	ctg	tta	att	cca	gct	cct	gat	gga	gga	ttt	1986
	Tyr	Thr	Trp	Ser	Arg	Pro	Leu	Leu	Ile	Pro	Ala	Pro	Asp	Gly	Gly	Phe	
		615					620					625					
	cct	gga	gggt	ccc	tct	cct	agc	gca	aat	act	ctc	tat	gct	gta	tggt	aat	2034
	Pro	Gly	Gly	Pro	Ser	Pro	Ser	Ala	Asn	Thr	Leu	Tyr	Ala	Val	Trp	Asn	
	630					635					640					645	
	tca	gac	act	ctc	gtg	cgt	tct	acc	tat	atc	tta	gat	ccc	gag	cgt	tac	2082
60	Ser	Asp	Thr	Leu	Val	Arg	Ser	Thr	Tyr	Ile	Leu	Asp	Pro	Glu	Arg	Tyr	
					650					655					660		

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	gga gaa att gtc agc aac agc tta tgg att tcc ttc tta gga aat cag	2130
	Gly Glu Ile Val Ser Asn Ser Leu Trp Ile Ser Phe Leu Gly Asn Gln	
	665 670 675	
	gca ttc tct gat att ctc caa gat gtt ctt ttg ata gat cat ccc ggg	2178
	Ala Phe Ser Asp Ile Leu Gln Asp Val Leu Leu Ile Asp His Pro Gly	
	680 685 690	
10	ttg tcc ata acc gcg aaa gct tta gga gcc tat gtc gaa cac aca cca	2226
	Leu Ser Ile Thr Ala Lys Ala Leu Gly Ala Tyr Val Glu His Thr Pro	
	695 700 705	
	aga caa gga cat gag ggc ttt tca ggt cgc tat gga ggc tac caa gct	2274
	Arg Gln Gly His Glu Gly Phe Ser Gly Arg Tyr Gly Gly Tyr Gln Ala	
	710 715 720 725	
20	gcg cta tct atg aac tac acg gac cac act acg tta gga ctt tct ttc	2322
	Ala Leu Ser Met Asn Tyr Thr Asp His Thr Thr Leu Gly Leu Ser Phe	
	730 735 740	
	ggg cag ctt tat gga aaa act aac gcc aac ccc tac gat tca cgt tgc	2370
	Gly Gln Leu Tyr Gly Lys Thr Asn Ala Asn Pro Tyr Asp Ser Arg Cys	
	745 750 755	
	tca gaa caa atg tat tta ctc tcg ttc ttt ggt caa ttc cct atc gtg	2418
	Ser Glu Gln Met Tyr Leu Leu Ser Phe Phe Gly Gln Phe Pro Ile Val	
	760 765 770	
30	act caa aag agc gag gcc tta att tcc tgg aaa gca gct tat ggt tat	2466
	Thr Gln Lys Ser Glu Ala Leu Ile Ser Trp Lys Ala Ala Tyr Gly Tyr	
	775 780 785	
	tcc aaa aat cac cta aat acc acc tac ctc aga cct gac aaa gct cca	2514
	Ser Lys Asn His Leu Asn Thr Thr Tyr Leu Arg Pro Asp Lys Ala Pro	
	790 795 800 805	
40	aaa tct caa ggg caa tgg cat aac aat agt tac tat gtt ctt att tct	2562
	Lys Ser Gln Gly Gln Trp His Asn Asn Ser Tyr Tyr Val Leu Ile Ser	
	810 815 820	
	gca gaa cat cct ttc cta aac tgg tgt ctt ctt aca aga cct ctg gct	2610
	Ala Glu His Pro Phe Leu Asn Trp Cys Leu Leu Thr Arg Pro Leu Ala	
	825 830 835	
	caa gct tgg gat ctt tca ggt ttt att tcc gca gaa ttc cta ggt ggt	2658
	Gln Ala Trp Asp Leu Ser Gly Phe Ile Ser Ala Glu Phe Leu Gly Gly	
	840 845 850	
50	tgg caa agt aag ttc aca gaa act gga gat ctg caa cgt agc ttt agt	2706
	Trp Gln Ser Lys Phe Thr Glu Thr Gly Asp Leu Gln Arg Ser Phe Ser	
	855 860 865	
	aga ggt aaa ggg tac aat gtt tcc cta ccg ata gga tgt tct tct caa	2754
	Arg Gly Lys Gly Tyr Asn Val Ser Leu Pro Ile Gly Cys Ser Ser Gln	
	870 875 880 885	
60	tgg ttc aca cca ttt aag aag gct cct tct aca ctg acc atc aaa ctt	2802
	Trp Phe Thr Pro Phe Lys Lys Ala Pro Ser Thr Leu Thr Ile Lys Leu	
	890 895 900	

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gcc tac aag cct gat atc tat cgt gtc aac cct cac aat att gtg act 2850
Ala Tyr Lys Pro Asp Ile Tyr Arg Val Asn Pro His Asn Ile Val Thr
                      905                      910                      915

gtc gtc tca aac caa gag agc act tcg atc tca gga gca aat cta cgc 2898
Val Val Ser Asn Gln Glu Ser Thr Ser Ile Ser Gly Ala Asn Leu Arg
                      920                      925                      930

10  cgc cac ggt ttg ttt gta caa atc cat gat gta gta gat ctc acc gag 2946
Arg His Gly Leu Phe Val Gln Ile His Asp Val Val Asp Leu Thr Glu
                      935                      940                      945

gac act cag gcc ttt cta aac tat acc ttt gac ggg aaa aat gga ttt 2994
Asp Thr Gln Ala Phe Leu Asn Tyr Thr Phe Asp Gly Lys Asn Gly Phe
950                      955                      960                      965

20  aca aac cac cga gtg tct aca gga cta aaa tcc aca ttt taaaactcta 3043
Thr Asn His Arg Val Ser Thr Gly Leu Lys Ser Thr Phe
                      970                      975

agctctgctt agagttttct gtagccccgg tcgtcttaga atcctctatc catcatcgaa 3103
gaacttagca atgaaggcca agattctcac tctatgagaa cccccc 3150

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<220>
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<222> (936)..(944)

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 1                      5

40  <210> 27
<211> 841
<212> PRT
<213> Chlamydia pneumoniae

<400> 27
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 1                      5                      10                      15

50  Ser Met Ser Asn Leu Leu Gly Ala Ala Thr Thr Glu Glu Leu Ser Ala
                20                      25                      30

Ser Asn Ser Phe Asp Gly Thr Thr Ser Thr Thr Ser Phe Ser Ser Lys
                35                      40                      45

Thr Ser Ser Ala Thr Asp Gly Thr Asn Tyr Val Phe Lys Asp Ser Val
 50                      55                      60

60  Val Ile Glu Asn Val Pro Lys Thr Gly Glu Thr Gln Ser Thr Ser Cys
    65                      70                      75                      80

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	Phe	Lys	Asn	Asp	Ala	Ala	Ala	Gly	Asp	Leu	Asn	Phe	Leu	Gly	Gly	Gly	
					85					90					95		
	Phe	Ser	Phe	Thr	Phe	Ser	Asn	Ile	Asp	Ala	Thr	Thr	Ala	Ser	Gly	Ala	
				100					105					110			
	Ala	Ile	Gly	Ser	Glu	Ala	Ala	Asn	Lys	Thr	Val	Thr	Leu	Ser	Gly	Phe	
			115					120					125				
10	Ser	Ala	Leu	Ser	Phe	Leu	Lys	Ser	Pro	Ala	Ser	Thr	Val	Thr	Asn	Gly	
		130					135					140					
	Leu	Gly	Ala	Ile	Asn	Val	Lys	Gly	Asn	Leu	Ser	Leu	Leu	Asp	Asn	Asp	
	145					150					155				160		
	Lys	Val	Leu	Ile	Gln	Asp	Asn	Phe	Ser	Thr	Gly	Asp	Gly	Gly	Ala	Ile	
				165						170					175		
20	Asn	Cys	Ala	Gly	Ser	Leu	Lys	Ile	Ala	Asn	Asn	Lys	Ser	Leu	Ser	Phe	
			180						185					190			
	Ile	Gly	Asn	Ser	Ser	Ser	Thr	Arg	Gly	Gly	Ala	Ile	His	Thr	Lys	Asn	
		195						200					205				
	Leu	Thr	Leu	Ser	Ser	Gly	Gly	Glu	Thr	Leu	Phe	Gln	Gly	Asn	Thr	Ala	
	210					215						220					
30	Pro	Thr	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Ala	Ile	Ala	Asp	Ser	Gly	
	225					230					235					240	
	Thr	Leu	Ser	Ile	Ser	Gly	Asp	Ser	Gly	Asp	Ile	Ile	Phe	Glu	Gly	Asn	
				245					250						255		
	Thr	Ile	Gly	Ala	Thr	Gly	Thr	Val	Ser	His	Ser	Ala	Ile	Asp	Leu	Gly	
			260					265						270			
	Thr	Ser	Ala	Lys	Ile	Thr	Ala	Leu	Arg	Ala	Ala	Gln	Gly	His	Thr	Ile	
		275						280					285				
40	Tyr	Phe	Tyr	Asp	Pro	Ile	Thr	Val	Thr	Gly	Ser	Thr	Ser	Val	Ala	Asp	
	290					295						300					
	Ala	Leu	Asn	Ile	Asn	Ser	Pro	Asp	Thr	Gly	Asp	Asn	Lys	Glu	Tyr	Thr	
	305					310					315				320		
	Gly	Thr	Ile	Val	Phe	Ser	Gly	Glu	Lys	Leu	Thr	Glu	Ala	Glu	Ala	Lys	
				325						330					335		
50	Asp	Glu	Lys	Asn	Arg	Thr	Ser	Lys	Leu	Leu	Gln	Asn	Val	Ala	Phe	Lys	
				340					345					350			
	Asn	Gly	Thr	Val	Val	Leu	Lys	Gly	Asp	Val	Val	Leu	Ser	Ala	Asn	Gly	
			355					360					365				
	Phe	Ser	Gln	Asp	Ala	Asn	Ser	Lys	Leu	Ile	Met	Asp	Leu	Gly	Thr	Ser	
		370					375					380					
60	Leu	Val	Ala	Asn	Thr	Glu	Ser	Ile	Glu	Leu	Thr	Asn	Leu	Glu	Ile	Asn	
	385				390						395					400	

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	Ile	Asp	Ser	Leu	Arg	Asn	Gly	Lys	Lys	Ile	Lys	Leu	Ser	Ala	Ala	Thr	
					405					410					415		
	Ala	Gln	Lys	Asp	Ile	Arg	Ile	Asp	Arg	Pro	Val	Val	Leu	Ala	Ile	Ser	
				420					425					430			
10	Asp	Glu	Ser	Phe	Tyr	Gln	Asn	Gly	Phe	Leu	Asn	Glu	Asp	His	Ser	Tyr	
			435					440					445				
	Asp	Gly	Ile	Leu	Glu	Leu	Asp	Ala	Gly	Lys	Asp	Ile	Val	Ile	Ser	Ala	
		450					455					460					
	Asp	Ser	Arg	Ser	Ile	Asp	Ala	Val	Gln	Ser	Pro	Tyr	Gly	Tyr	Gln	Gly	
	465					470					475					480	
	Lys	Trp	Thr	Ile	Asn	Trp	Ser	Thr	Asp	Asp	Lys	Lys	Ala	Thr	Val	Ser	
					485					490					495		
20	Trp	Ala	Lys	Gln	Ser	Phe	Asn	Pro	Thr	Ala	Glu	Gln	Glu	Ala	Pro	Leu	
				500					505					510			
	Val	Pro	Asn	Leu	Leu	Trp	Gly	Ser	Phe	Ile	Asp	Val	Arg	Ser	Phe	Gln	
			515					520					525				
	Asn	Phe	Ile	Glu	Leu	Gly	Thr	Glu	Gly	Ala	Pro	Tyr	Glu	Lys	Arg	Phe	
		530					535					540					
30	Trp	Val	Ala	Gly	Ile	Ser	Asn	Val	Leu	His	Arg	Ser	Gly	Arg	Glu	Asn	
	545					550					555					560	
	Gln	Arg	Lys	Phe	Arg	His	Val	Ser	Gly	Gly	Ala	Val	Val	Gly	Ala	Ser	
				565						570					575		
	Thr	Arg	Met	Pro	Gly	Gly	Asp	Thr	Leu	Ser	Leu	Gly	Phe	Ala	Gln	Leu	
				580					585					590			
	Phe	Ala	Arg	Asp	Lys	Asp	Tyr	Phe	Met	Asn	Thr	Asn	Phe	Ala	Lys	Thr	
40			595					600					605				
	Tyr	Ala	Gly	Ser	Leu	Arg	Leu	Gln	His	Asp	Ala	Ser	Leu	Tyr	Ser	Val	
		610					615					620					
	Val	Ser	Ile	Leu	Leu	Gly	Glu	Gly	Gly	Leu	Arg	Glu	Ile	Leu	Leu	Pro	
	625					630					635					640	
	Tyr	Val	Ser	Lys	Thr	Leu	Pro	Cys	Ser	Phe	Tyr	Gly	Gln	Leu	Ser	Tyr	
				645						650				655			
50	Gly	His	Thr	Asp	His	Arg	Met	Lys	Thr	Glu	Ser	Leu	Pro	Pro	Pro	Pro	
				660					665					670			
	Pro	Thr	Leu	Ser	Thr	Asp	His	Thr	Ser	Trp	Gly	Gly	Tyr	Val	Trp	Ala	
				675				680					685				
	Gly	Glu	Leu	Gly	Thr	Arg	Val	Ala	Val	Glu	Asn	Thr	Ser	Gly	Arg	Gly	
		690					695					700					
60	Phe	Phe	Gln	Glu	Tyr	Thr	Pro	Phe	Val	Lys	Val	Gln	Ala	Val	Tyr	Ala	
	705					710					715					720	

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Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser  
 725 730 735  
 Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu  
 740 745 750  
 10 Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro  
 755 760 765  
 Asp Val Cys Arg Ser Asn Pro Lys Cys Thr Thr Thr Leu Leu Ser Asn  
 770 775 780  
 Gln Gly Ser Trp Lys Thr Lys Gly Ser Asn Leu Ala Arg Gln Ala Gly  
 785 790 795 800  
 Ile Val Gln Ala Ser Gly Phe Arg Ser Leu Gly Ala Ala Ala Glu Leu  
 805 810 815  
 20 Phe Gly Asn Phe Gly Phe Glu Trp Arg Gly Ser Ser Arg Ser Tyr Asn  
 820 825 830  
 Val Asp Ala Gly Ser Lys Ile Lys Phe  
 835 840  
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 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 28  
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 1 5 10 15  
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 20 25 30  
 40 Ser Asn Ser Phe Asp Gly Thr Thr Ser Thr Thr Ser Phe Ser Ser Lys  
 35 40 45  
 Thr Ser Ser Ala Thr Asp Gly Thr Asn Tyr Val Phe Lys Asp Ser Val  
 50 55 60  
 Val Ile Glu Asn Val Pro Lys Thr Gly Glu Thr Gln Ser Thr Ser Cys  
 65 70 75 80  
 50 Phe Lys Asn Asp Ala Ala Ala Gly Asp Leu Asn Phe Leu Gly Gly Gly  
 85 90 95  
 Phe Ser Phe Thr Phe Ser Asn Ile Asp Ala Thr Thr Ala Ser Gly Ala  
 100 105 110  
 Ala Ile Gly Ser Glu Ala Ala Asn Lys Thr Val Thr Leu Ser Gly Phe  
 115 120 125  
 Ser Ala Leu Ser Phe Leu Lys Ser Pro Ala Ser Thr Val Thr Asn Gly  
 130 135 140  
 60

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	Leu	Gly	Ala	Ile	Asn	Val	Lys	Gly	Asn	Leu	Ser	Leu	Leu	Asp	Asn	Asp	
	145					150					155					160	
	Lys	Val	Leu	Ile	Gln	Asp	Asn	Phe	Ser	Thr	Gly	Asp	Gly	Gly	Ala	Ile	
					165					170					175		
10	Asn	Cys	Ala	Gly	Ser	Leu	Lys	Ile	Ala	Asn	Asn	Lys	Ser	Leu	Ser	Phe	
				180					185					190			
	Ile	Gly	Asn	Ser	Ser	Ser	Thr	Arg	Gly	Gly	Ala	Ile	His	Thr	Lys	Asn	
			195					200					205				
	Leu	Thr	Leu	Ser	Ser	Gly	Gly	Glu	Thr	Leu	Phe	Gln	Gly	Asn	Thr	Ala	
	210						215					220					
	Pro	Thr	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Ala	Ile	Ala	Asp	Ser	Gly	
	225					230					235					240	
20	Thr	Leu	Ser	Ile	Ser	Gly	Asp	Ser	Gly	Asp	Ile	Ile	Phe	Glu	Gly	Asn	
					245					250					255		
	Thr	Ile	Gly	Ala	Thr	Gly	Thr	Val	Ser	His	Ser	Ala	Ile	Asp	Leu	Gly	
				260					265					270			
	Thr	Ser	Ala	Lys	Ile	Thr	Ala	Leu	Arg	Ala	Ala	Gln	Gly	His	Thr	Ile	
			275					280					285				
30	Tyr	Phe	Tyr	Asp	Pro	Ile	Thr	Val	Thr	Gly	Ser	Thr	Ser	Val	Ala	Asp	
		290					295					300					
	Ala	Leu	Asn	Ile	Asn	Ser	Pro	Asp	Thr	Gly	Asp	Asn	Lys	Glu	Tyr	Thr	
	305					310					315					320	
	Gly	Thr	Ile	Val	Phe	Ser	Gly	Glu	Lys	Leu	Thr	Glu	Ala	Glu	Ala	Lys	
					325					330					335		
40	Asp	Glu	Lys	Asn	Arg	Thr	Ser	Lys	Leu	Leu	Gln	Asn	Val	Ala	Phe	Lys	
				340					345					350			
	Asn	Gly	Thr	Val	Val	Leu	Lys	Gly	Asp	Val	Val	Leu	Ser	Ala	Asn	Gly	
			355					360					365				
	Phe	Ser	Gln	Asp	Ala	Asn	Ser	Lys	Leu	Ile	Met	Asp	Leu	Gly	Thr	Ser	
		370					375					380					
	Leu	Val	Ala	Asn	Thr	Glu	Ser	Ile	Glu	Leu	Thr	Asn	Leu	Glu	Ile	Asn	
	385				390						395					400	
50	Ile	Asp	Ser	Leu	Arg	Asn	Gly	Lys	Lys	Ile	Lys	Leu	Ser	Ala	Ala	Thr	
					405					410					415		
	Ala	Gln	Lys	Asp	Ile	Arg	Ile	Asp	Arg	Pro	Val	Val	Leu	Ala	Ile	Ser	
				420				425						430			
	Asp	Glu	Ser	Phe	Tyr	Gln	Asn	Gly	Phe	Leu	Asn	Glu	Asp	His	Ser	Tyr	
			435					440					445				
60	Asp	Gly	Ile	Leu	Glu	Leu	Asp	Ala	Gly	Lys	Asp	Ile	Val	Ile	Ser	Ala	
		450					455					460					

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	Asp	Ser	Arg	Ser	Ile	Asp	Ala	Val	Gln	Ser	Pro	Tyr	Gly	Tyr	Gln	Gly	
	465					470					475					480	
	Lys	Trp	Thr	Ile	Asn	Trp	Ser	Thr	Asp	Asp	Lys	Lys	Ala	Thr	Val	Ser	
					485					490					495		
10	Trp	Ala	Lys	Gln	Ser	Phe	Asn	Pro	Thr	Ala	Glu	Gln	Glu	Ala	Pro	Leu	
				500					505					510			
	Val	Pro	Asn	Leu	Leu	Trp	Gly	Ser	Phe	Ile	Asp	Val	Arg	Ser	Phe	Gln	
			515					520					525				
	Asn	Phe	Ile	Glu	Leu	Gly	Thr	Glu	Gly	Ala	Pro	Tyr	Glu	Lys	Arg	Phe	
		530					535					540					
	Trp	Val	Ala	Gly	Ile	Ser	Asn	Val	Leu	His	Arg	Ser	Gly	Arg	Glu	Asn	
	545					550					555					560	
20	Gln	Arg	Lys	Phe	Arg	His	Val	Ser	Gly	Gly	Ala	Val	Val	Gly	Ala	Ser	
					565					570					575		
	Thr	Arg	Met	Pro	Gly	Gly	Asp	Thr	Leu	Ser	Leu	Gly	Phe	Ala	Gln	Leu	
				580					585						590		
	Phe	Ala	Arg	Asp	Lys	Asp	Tyr	Phe	Met	Asn	Thr	Asn	Phe	Ala	Lys	Thr	
			595					600					605				
30	Tyr	Ala	Gly	Ser	Leu	Arg	Leu	Gln	His	Asp	Ala	Ser	Leu	Tyr	Ser	Val	
		610					615					620					
	Val	Ser	Ile	Leu	Leu	Gly	Glu	Gly	Gly	Leu	Arg	Glu	Ile	Leu	Leu	Pro	
	625					630					635					640	
	Tyr	Val	Ser	Lys	Thr	Leu	Pro	Cys	Ser	Phe	Tyr	Gly	Gln	Leu	Ser	Tyr	
					645					650					655		
40	Gly	His	Thr	Asp	His	Arg	Met	Lys	Thr	Glu	Ser	Leu	Pro	Pro	Pro	Pro	
				660					665					670			
	Pro	Thr	Leu	Ser	Thr	Asp	His	Thr	Ser	Trp	Gly	Gly	Tyr	Val	Trp	Ala	
			675					680					685				
	Gly	Glu	Leu	Gly	Thr	Arg	Val	Ala	Val	Glu	Asn	Thr	Ser	Gly	Arg	Gly	
		690					695					700					
	Phe	Phe	Gln	Glu	Tyr	Thr	Pro	Phe	Val	Lys	Val	Gln	Ala	Val	Tyr	Ala	
	705					710					715					720	
50	Arg	Gln	Asp	Ser	Phe	Val	Glu	Leu	Gly	Ala	Ile	Ser	Arg	Asp	Phe	Ser	
					725					730					735		
	Asp	Ser	His	Leu	Tyr	Asn	Leu	Ala	Ile	Pro	Leu	Gly	Ile	Lys	Leu	Glu	
				740					745					750			
	Lys	Arg	Phe	Ala	Glu	Gln	Tyr	Tyr	His	Val	Val	Ala	Met	Tyr	Ser	Pro	
			755					760					765				
60	Asp	Val	Cys	Arg	Ser	Asn	Pro	Lys	Cys	Thr	Thr	Thr	Leu	Leu	Ser	Asn	
		770					775					780					



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Gln Gly Ser Trp Lys Thr Lys Gly Ser Asn Leu Ala Arg Gln Ala Gly  
 785 790 795 800  
 Ile Val Gln Ala Ser Gly Phe Arg Ser Leu Gly Ala Ala Ala Glu Leu  
 805 810 815  
 10 Phe Gly Asn Phe Gly Phe Glu Trp Arg Gly Ser Ser Arg Ser Tyr Asn  
 820 825 830  
 Val Asp Ala Gly Ser Lys Ile Lys Phe  
 835 840  
 <210> 29  
 <211> 245  
 <212> PRT  
 <213> Chlamydia pneumoniae  
 20 <400> 29  
 Met Pro Pro Leu Asn Ala Asp Asp Val Leu Pro Arg Asp His Leu Ser  
 1 5 10 15  
 Asp Gly Ser Phe Ser Asp Thr Tyr Pro Asp Ile Thr Thr Gln Ala Ile  
 20 25 30  
 30 Ile Leu Ile Phe Leu Ala Leu Ser Pro Phe Leu Val Met Leu Leu Thr  
 35 40 45  
 Ser Tyr Leu Lys Ile Ile Ile Thr Leu Val Leu Leu Arg Asn Ala Leu  
 50 55 60  
 Gly Val Gln Gln Thr Pro Pro Ser Gln Val Leu Asn Gly Ile Ala Leu  
 65 70 75 80  
 Ile Leu Ser Ile Tyr Val Met Phe Pro Thr Gly Val Ala Met Tyr Lys  
 85 90 95  
 40 Asp Ala Arg Lys Glu Ile Glu Ala Asn Thr Ile Pro Gln Ser Leu Phe  
 100 105 110  
 Thr Ala Glu Gly Ala Glu Thr Val Phe Val Ala Leu Asn Lys Ser Lys  
 115 120 125  
 Glu Pro Leu Arg Ser Phe Leu Ile Arg Asn Thr Pro Lys Ala Gln Ile  
 130 135 140  
 50 Gln Ser Phe Tyr Lys Ile Ser Gln Lys Thr Phe Pro Ser Glu Ile Arg  
 145 150 155 160  
 Ala His Leu Thr Ala Ser Asp Phe Val Ile Ile Ile Pro Ala Phe Ile  
 165 170 175  
 Met Gly Gln Ile Lys Asn Ala Phe Glu Ile Gly Val Leu Ile Tyr Leu  
 180 185 190  
 Pro Phe Phe Val Ile Asp Leu Val Thr Ala Asn Val Leu Val Ala Met  
 195 200 205  
 60

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Gln Met Met Met Leu Ser Pro Leu Ser Ile Ser Leu Pro Leu Lys Leu  
 210 215 220

Leu Leu Ile Val Met Val Asp Gly Trp Thr Leu Leu Leu Gln Gly Leu  
 225 230 235 240

10 Met Ile Ser Phe Lys  
 245

<210> 30

<211> 233

<212> PRT

<213> Chlamydia pneumoniae

<400> 30

20 Met Lys Phe Phe Ser Leu Ile Phe Lys Asp Asp Asp Val Ser Pro Asn  
 1 5 10 15

Lys Lys Val Leu Ser Pro Glu Ala Phe Ser Ala Phe Leu Asp Ala Lys  
 20 25 30

Glu Leu Leu Glu Lys Thr Lys Ala Asp Ser Glu Ala Tyr Val Ala Glu  
 35 40 45

30 Thr Glu Gln Lys Cys Ala Gln Ile Arg Gln Glu Ala Lys Asp Gln Gly  
 50 55 60

Phe Lys Glu Gly Ser Glu Ser Trp Ser Lys Gln Ile Ala Phe Leu Glu  
 65 70 75 80

Glu Glu Thr Lys Asn Leu Arg Ile Arg Val Arg Glu Ala Leu Val Pro  
 85 90 95

Leu Ala Ile Ala Ser Val Arg Lys Ile Ile Gly Lys Glu Leu Glu Leu  
 100 105 110

40 His Pro Glu Thr Ile Val Ser Ile Ile Ser Gln Ala Leu Lys Glu Leu  
 115 120 125

Thr Gln Asn Lys His Ile Ile Ile Ser Val Asn Pro Lys Asp Leu Pro  
 130 135 140

Leu Val Glu Lys Ser Arg Pro Glu Leu Lys Asn Ile Val Glu Tyr Ala  
 145 150 155 160

50 Asp Ser Leu Ile Leu Thr Ala Lys Pro Asp Val Thr Pro Gly Gly Cys  
 165 170 175

Ile Ile Glu Thr Glu Ala Gly Ile Ile Asn Ala Gln Leu Asp Val Gln  
 180 185 190

Leu Asp Ala Leu Glu Lys Ala Phe Ser Thr Ile Leu Lys Ala Lys Asn  
 195 200 205

60 Pro Val Asp Glu Pro Ser Glu Thr Ser Ser Ser Thr Asp Ser Ser Ser  
 210 215 220

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Leu Ser Asn Asp Gln Asp Lys Lys Glu  
 225 230

<210> 31  
 <211> 322  
 <212> PRT

10 <213> Chlamydia pneumoniae

<400> 31

Met Thr Leu Leu Cys Cys Thr Ser Cys Asn Ser Arg Ser Leu Ile Val  
 1 5 10 15

His Gly Leu Pro Gly Arg Glu Ala Asn Glu Ile Val Val Leu Leu Val  
 20 25 30

20 Ser Lys Gly Val Ala Ala Gln Lys Leu Pro Gln Ala Ala Ala Ala Thr  
 35 40 45

Ala Gly Ala Ala Thr Glu Gln Met Trp Asp Ile Ala Val Pro Ser Ala  
 50 55 60

Gln Ile Thr Glu Ala Leu Ala Ile Leu Asn Gln Ala Gly Leu Pro Arg  
 65 70 75 80

30 Met Lys Gly Thr Ser Leu Leu Asp Leu Phe Ala Lys Gln Gly Leu Val  
 85 90 95

Pro Ser Glu Leu Gln Glu Lys Ile Arg Tyr Gln Glu Gly Leu Ser Glu  
 100 105 110

Gln Met Ala Ser Thr Ile Arg Lys Met Asp Gly Val Val Asp Ala Ser  
 115 120 125

Val Gln Ile Ser Phe Thr Thr Glu Asn Glu Asp Asn Leu Pro Leu Thr  
 130 135 140

40 Ala Ser Val Tyr Ile Lys His Arg Gly Val Leu Asp Asn Pro Asn Ser  
 145 150 155 160

Ile Met Val Ser Lys Ile Lys Arg Leu Ile Ala Ser Ala Val Pro Gly  
 165 170 175

Leu Val Pro Glu Asn Val Ser Val Val Ser Asp Arg Ala Ala Tyr Ser  
 180 185 190

50 Asp Ile Thr Ile Asn Gly Pro Trp Gly Leu Thr Glu Glu Ile Asp Tyr  
 195 200 205

Val Ser Val Trp Gly Ile Ile Leu Ala Lys Ser Ser Leu Thr Lys Phe  
 210 215 220

Arg Leu Ile Phe Tyr Val Leu Ile Leu Ile Leu Phe Val Ile Ser Cys  
 225 230 235 240

Gly Leu Leu Trp Val Ile Trp Lys Thr His Thr Leu Ile Met Thr Met  
 245 250 255

60

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Gly Gly Thr Lys Gly Phe Phe Asn Pro Thr Pro Tyr Thr Lys Asn Ala  
 260 265 270  
 Leu Glu Ala Lys Lys Ala Glu Gly Ala Ala Ala Asp Lys Glu Lys Lys  
 275 280 285  
 10 Glu Asp Ala Asp Ser Gln Gly Glu Ser Lys Asn Ala Glu Thr Ser Asp  
 290 295 300  
 Lys Asp Ser Ser Asp Lys Asp Ala Pro Glu Gly Ser Asn Glu Ile Glu  
 305 310 315 320  
 Gly Ala  
 <210> 32  
 <211> 226  
 20 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 32  
 Met Thr Ile Arg Val Arg Asn Leu Ala Tyr Ser Val Asn Lys Lys Lys  
 1 5 10 15  
 Ile Leu Asp Gly Val Thr Phe Ser Leu Glu Arg Gly His Ile Thr Leu  
 20 25 30  
 30 Phe Val Gly Lys Ser Gly Ser Gly Lys Thr Met Ile Leu Arg Ala Leu  
 35 40 45  
 Ala Gly Leu Val Gln Pro Thr Gln Gly Asp Ile Trp Ile Glu Gly Glu  
 50 55 60  
 Ala Pro Ala Leu Val Phe Gln Gln Pro Glu Leu Phe Ser His Met Thr  
 65 70 75 80  
 40 Val Leu Gly Asn Cys Thr His Pro Gln Ile His Ile Lys Gly Arg Ser  
 85 90 95  
 Thr Glu Glu Ala Arg Glu Lys Ala Phe Glu Leu Leu His Leu Leu Asp  
 100 105 110  
 Ile Glu Glu Val Ala Lys Asn Tyr Pro Asp Gln Leu Ser Gly Gly Gln  
 115 120 125  
 Lys Gln Arg Val Ala Ile Val Arg Ser Leu Cys Met Asp Lys His Thr  
 130 135 140  
 50 Leu Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Phe Ala Thr Ala  
 145 150 155 160  
 Ser Phe Arg His Leu Leu Glu Thr Leu Arg Asp Gln Glu Leu Thr Val  
 165 170 175  
 Gly Leu Thr Thr His Asp Met Gln Phe Val His Ser Cys Leu Asp Arg  
 180 185 190  
 60 Ile Tyr Leu Ile Asp Gln Gly Thr Val Ala Gly Val Tyr Asp Lys Arg  
 195 200 205

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Asp Gly Glu Leu Asp Ser Gly His Pro Leu Ser Lys Tyr Ile His Ser  
 210 215 220

Ala Gln  
 225

10 <210> 33  
 <211> 436  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 33  
 Met Lys Arg Pro Phe Phe Thr Tyr Leu Cys Ile Ile Phe Tyr Gly Ser  
 1 5 10 15

20 Cys Ala Ser Leu Ser Leu His Ala Gly Leu Ser Phe Pro Glu Val Arg  
 20 25 30

Gly Ala Thr Ala Ala Val Val His Ala Asp Ser Gly Lys Val Phe Tyr  
 35 40 45

Asp Lys Asp Ile Asp Ala Val Ile Tyr Pro Ala Ser Met Thr Lys Ile  
 50 55 60

30 Ala Thr Ala Leu Phe Ile Leu Lys His Tyr Pro Thr Val Leu Asp Thr  
 65 70 75 80

Leu Ile Lys Val Lys Gln Asp Ala Ile Ala Ser Ile Thr Pro Gln Ala  
 85 90 95

Lys Lys Gln Ser Gly Tyr Arg Ser Pro Pro His Trp Leu Glu Thr Asp  
 100 105 110

Gly Ser Thr Ile Gln Leu His Leu Arg Glu Glu Leu Leu Gly Trp Asp  
 115 120 125

40 Leu Phe His Ala Leu Leu Val Cys Ser Ala Asn Asp Ala Ala Asn Val  
 130 135 140

Leu Ala Met Ala Cys Cys Gly Ser Val Glu Lys Phe Met Asp Lys Leu  
 145 150 155 160

Asn Phe Phe Leu Lys Glu Glu Ile Gly Cys Thr His Thr His Phe Asn  
 165 170 175

50 Asn Pro His Gly Leu His His Pro Asn His Tyr Thr Thr Thr Arg Asp  
 180 185 190

Leu Ile Ser Ile Met Arg Cys Ala Leu Lys Glu Pro Pro Phe Arg Gly  
 195 200 205

Val Ile Ser Thr Thr Ser Tyr Lys Ile Gly Ala Thr Asn Leu His Gly  
 210 215 220

Glu Arg Ile Leu Ser Pro Thr Asn Lys Leu Leu Leu Pro Gly Ser Thr  
 225 230 235 240

60



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Lys Lys Gln Ser Gly Tyr Arg Ser Pro Pro His Trp Leu Glu Thr Asp  
 60 65 70 75  
 Gly Ser Thr Ile Gln Leu His Leu Arg Glu Glu Leu Leu Gly Trp Asp  
 80 85 90  
 10 Leu Phe His Ala Leu Leu Val Cys Ser Ala Asn Asp Ala Ala Asn Val  
 95 100 105  
 Leu Ala Met Ala Cys Cys Gly Ser Val Glu Lys Phe Met Asp Lys Leu  
 110 115 120  
 Asn Phe Phe Leu Lys Glu Glu Ile Gly Cys Thr His Thr His Phe Asn  
 125 130 135  
 20 Asn Pro His Gly Leu His His Pro Asn His Tyr Thr Thr Thr Arg Asp  
 140 145 150 155  
 Leu Ile Ser Ile Met Arg Cys Ala Leu Lys Glu Pro Pro Phe Arg Gly  
 160 165 170  
 Val Ile Ser Thr Thr Ser Tyr Lys Ile Gly Ala Thr Asn Leu His Gly  
 175 180 185  
 Glu Arg Ile Leu Ser Pro Thr Asn Lys Leu Leu Leu Pro Gly Ser Thr  
 190 195 200  
 30 Tyr His Tyr Pro Pro Ala Leu Gly Gly Lys Thr Gly Thr Thr Lys Thr  
 205 210 215  
 Ala Gly Lys Asn Leu Ile Met Ala Ala Glu Lys Asn Asn Arg Leu Leu  
 220 225 230 235  
 Val Thr Ile Ala Thr Gly Tyr Ser Gly Pro  
 240 245  
 40 <210> 35  
 <211> 645  
 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 35  
 Met Ala Ser Asn Pro Ile Leu Gln Ile Glu Asp Leu Ser Ile Thr Leu  
 1 5 10 15  
 50 Ala Lys Gln Arg Gln Gln Tyr Pro Ile Val Gln Ser Leu Ser Phe Thr  
 20 25 30  
 Ile Asn Glu Gly Gln Thr Leu Ala Ile Ile Gly Glu Ser Gly Ser Gly  
 35 40 45  
 Lys Ser Val Ser Ala His Ala Ile Leu Arg Leu Leu Pro Cys Pro Pro  
 50 55 60  
 60 Phe Ser Val Ser Gly Gln Val Asn Phe Gln Gly His Asn Leu Leu Thr  
 65 70 75 80

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	Ala	Ser	Arg	Ser	Ile	Gln	Lys	Lys	Ile	Ile	Gly	Thr	Glu	Ile	Ser	Met	
					85					90					95		
	Ile	Phe	Gln	Asn	Pro	Gln	Ala	Ser	Leu	Asn	Pro	Val	Phe	Thr	Ile	Glu	
				100					105					110			
10	Gln	Gln	Phe	Arg	Glu	Ile	Ile	His	Thr	His	Leu	Ala	Leu	Thr	Ala	Glu	
			115					120					125				
	Val	Ala	Lys	Glu	Lys	Met	Leu	Tyr	Ala	Leu	Glu	Glu	Thr	Gly	Phe	His	
		130					135					140					
	Asp	Pro	Arg	Leu	Cys	Leu	Asn	Leu	Tyr	Pro	His	Gln	Leu	Ser	Gly	Gly	
	145					150					155					160	
	Met	Leu	Gln	Arg	Ile	Cys	Ile	Ala	Met	Ala	Leu	Leu	Cys	Ser	Pro	Lys	
					165				170						175		
20	Leu	Leu	Ile	Ala	Asp	Glu	Pro	Thr	Thr	Ala	Leu	Asp	Val	Ser	Val	Gln	
				180					185					190			
	Tyr	Gln	Ile	Leu	Gln	Leu	Leu	Lys	Thr	Leu	Gln	Lys	Lys	Thr	Gly	Met	
		195						200					205				
	Ser	Leu	Leu	Ile	Ile	Thr	His	Asn	Met	Gly	Val	Val	Ala	Glu	Thr	Ala	
		210					215					220					
30	Asp	Asp	Val	Leu	Val	Leu	Tyr	Ala	Gly	Arg	Met	Val	Glu	Cys	Ala	Pro	
	225					230					235				240		
	Ala	Val	Gln	Met	Phe	His	Asn	Pro	Ser	His	Pro	Tyr	Thr	Arg	Asp	Leu	
				245						250					255		
	Leu	Ala	Ser	Arg	Pro	Ser	Leu	Gln	Pro	Gln	Gln	Leu	Gly	Ser	Phe	Asn	
				260					265					270			
40	Pro	Ile	Pro	Gly	Gln	Pro	Pro	His	Tyr	Thr	Ala	Phe	Pro	Ser	Gly	Cys	
		275						280					285				
	Arg	Tyr	His	Pro	Arg	Cys	Ser	Lys	Ile	Leu	Asn	Arg	Cys	Ser	Ala	Glu	
		290				295						300					
	Ala	Pro	Glu	Ile	Tyr	Pro	Val	Arg	Glu	Gly	His	Lys	Val	Arg	Val	Gly	
	305					310					315					320	
	Cys	Met	Thr	Thr	Asn	Phe	Pro	Gln	Pro	Leu	Ile	Gln	Ala	Thr	Ser	Leu	
					325					330					335		
50	Thr	Lys	His	Tyr	Tyr	Lys	Arg	Ser	Phe	Trp	Phe	Gln	Gly	Lys	Thr	Ile	
				340					345					350			
	Ala	Ser	Arg	Pro	Val	Asp	Asp	Val	Ser	Phe	Ser	Leu	Tyr	Ser	Arg	Arg	
			355					360					365				
	Ala	Val	Gly	Leu	Ile	Gly	Glu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Ala	
			370				375					380					
60	Leu	Ala	Leu	Ala	Gly	Leu	Leu	Pro	Leu	Thr	Ser	Gly	Phe	Leu	Thr	Phe	
	385					390					395					400	



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Asn Gly Thr Pro Ile Lys Leu His Ser Lys His Gly Arg His Gln Leu  
 405 410 415  
 Arg Ser Gln Val Arg Leu Val Phe Gln Asn Pro Gln Ala Ser Leu Asn  
 420 425 430  
 10 Pro Arg Lys Thr Ile Leu Asp Ser Leu Gly His Ser Leu Leu Tyr His  
 435 440 445  
 Lys Leu Val Pro Lys Glu Lys Val Leu Ala Thr Val Arg Glu Tyr Leu  
 450 455 460  
 Glu Leu Val Gly Leu Ser Glu Glu Tyr Phe Tyr Arg Tyr Pro His Gln  
 465 470 475 480  
 Leu Ser Gly Gly Gln Gln Gln Arg Val Ser Ile Ala Arg Ala Leu Leu  
 485 490 495  
 20 Gly Val Pro Gln Leu Ile Ile Cys Asp Glu Ile Val Ser Ala Leu Asp  
 500 505 510  
 Leu Ser Ile Gln Ala Gln Ile Leu Asn Met Leu Ala Glu Leu Gln Lys  
 515 520 525  
 Lys Leu Ser Leu Thr Tyr Leu Phe Ile Ser His Asp Leu Ala Val Val  
 530 535 540  
 30 Arg Ser Phe Cys Thr Glu Val Phe Ile Met Tyr Lys Gly Gln Ile Val  
 545 550 555 560  
 Glu Lys Gly Asn Thr Lys Arg Ile Phe Ser Asp Pro Gln His Pro Tyr  
 565 570 575  
 Thr Arg Met Leu Leu Asn Ala Gln Leu Pro Glu Thr Pro Asp Gln Arg  
 580 585 590  
 40 Gln Ser Lys Pro Ile Phe Gln Glu Tyr His Lys Asp Ser Glu Glu Ser  
 595 600 605  
 Cys Ser Thr Gly Cys Tyr Phe Tyr Asn Arg Cys Pro Gln Lys Gln Glu  
 610 615 620  
 Ala Cys Lys Ser Glu Ile Ile Pro Asn Gln Gly Asp Ala His His Thr  
 625 630 635 640  
 Tyr Arg Cys Ile His  
 645  
 50

<210> 36  
 <211> 588  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 36  
 Ile Leu Gln Ile Glu Asp Leu Ser Ile Thr Leu  
 1 5 10

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	Ala	Lys	Gln	Arg	Gln	Gln	Tyr	Pro	Ile	Val	Gln	Ser	Leu	Ser	Phe	Thr	
				15					20					25			
	Ile	Asn	Glu	Gly	Gln	Thr	Leu	Ala	Ile	Ile	Gly	Glu	Ser	Gly	Ser	Gly	
			30					35					40				
10	Lys	Ser	Val	Ser	Ala	His	Ala	Ile	Leu	Arg	Leu	Leu	Pro	Cys	Pro	Pro	
		45					50					55					
	Phe	Ser	Val	Ser	Gly	Gln	Val	Asn	Phe	Gln	Gly	His	Asn	Leu	Leu	Thr	
	60					65					70					75	
	Ala	Ser	Arg	Ser	Ile	Gln	Lys	Lys	Ile	Ile	Gly	Thr	Glu	Ile	Ser	Met	
					80					85					90		
	Ile	Phe	Gln	Asn	Pro	Gln	Ala	Ser	Leu	Asn	Pro	Val	Phe	Thr	Ile	Glu	
				95					100					105			
20	Gln	Gln	Phe	Arg	Glu	Ile	Ile	His	Thr	His	Leu	Ala	Leu	Thr	Ala	Glu	
			110					115					120				
	Val	Ala	Lys	Glu	Lys	Met	Leu	Tyr	Ala	Leu	Glu	Glu	Thr	Gly	Phe	His	
		125					130					135					
	Asp	Pro	Arg	Leu	Cys	Leu	Asn	Leu	Tyr	Pro	His	Gln	Leu	Ser	Gly	Gly	
	140					145					150					155	
30	Met	Leu	Gln	Arg	Ile	Cys	Ile	Ala	Met	Ala	Leu	Leu	Cys	Ser	Pro	Lys	
					160					165					170		
	Leu	Leu	Ile	Ala	Asp	Glu	Pro	Thr	Thr	Ala	Leu	Asp	Val	Ser	Val	Gln	
				175					180						185		
	Tyr	Gln	Ile	Leu	Gln	Leu	Leu	Lys	Thr	Leu	Gln	Lys	Lys	Thr	Gly	Met	
			190					195					200				
	Ser	Leu	Leu	Ile	Ile	Thr	His	Asn	Met	Gly	Val	Val	Ala	Glu	Thr	Ala	
40		205					210					215					
	Asp	Asp	Val	Leu	Val	Leu	Tyr	Ala	Gly	Arg	Met	Val	Glu	Cys	Ala	Pro	
	220					225					230					235	
	Ala	Val	Gln	Met	Phe	His	Asn	Pro	Ser	His	Pro	Tyr	Thr	Arg	Asp	Leu	
					240					245					250		
	Leu	Ala	Ser	Arg	Pro	Ser	Leu	Gln	Pro	Gln	Gln	Leu	Gly	Ser	Phe	Asn	
				255					260					265			
50	Pro	Ile	Pro	Gly	Gln	Pro	Pro	His	Tyr	Thr	Ala	Phe	Pro	Ser	Gly	Cys	
			270					275						280			
	Arg	Tyr	His	Pro	Arg	Cys	Ser	Lys	Ile	Leu	Asn	Arg	Cys	Ser	Ala	Glu	
		285					290					295					
	Ala	Pro	Glu	Ile	Tyr	Pro	Val	Arg	Glu	Gly	His	Lys	Val	Arg	Val	Gly	
	300					305					310					315	
60	Cys	Met	Thr	Thr	Asn	Phe	Pro	Gln	Pro	Leu	Ile	Gln	Ala	Thr	Ser	Leu	
					320					325					330		

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Thr Lys His Tyr Tyr Lys Arg Ser Phe Trp Phe Gln Gly Lys Thr Ile  
 335 340 345  
 Ala Ser Arg Pro Val Asp Asp Val Ser Phe Ser Leu Tyr Ser Arg Arg  
 350 355 360  
 10 Ala Val Gly Leu Ile Gly Glu Ser Gly Ser Gly Lys Ser Thr Leu Ala  
 365 370 375  
 Leu Ala Leu Ala Gly Leu Leu Pro Leu Thr Ser Gly Phe Leu Thr Phe  
 380 385 390 395  
 Asn Gly Thr Pro Ile Lys Leu His Ser Lys His Gly Arg His Gln Leu  
 400 405 410  
 Arg Ser Gln Val Arg Leu Val Phe Gln Asn Pro Gln Ala Ser Leu Asn  
 415 420 425  
 20 Pro Arg Lys Thr Ile Leu Asp Ser Leu Gly His Ser Leu Leu Tyr His  
 430 435 440  
 Lys Leu Val Pro Lys Glu Lys Val Leu Ala Thr Val Arg Glu Tyr Leu  
 445 450 455  
 Glu Leu Val Gly Leu Ser Glu Glu Tyr Phe Tyr Arg Tyr Pro His Gln  
 460 465 470 475  
 30 Leu Ser Gly Gly Gln Gln Gln Arg Val Ser Ile Ala Arg Ala Leu Leu  
 480 485 490  
 Gly Val Pro Gln Leu Ile Ile Cys Asp Glu Ile Val Ser Ala Leu Asp  
 495 500 505  
 Leu Ser Ile Gln Ala Gln Ile Leu Asn Met Leu Ala Glu Leu Gln Lys  
 510 515 520  
 40 Lys Leu Ser Leu Thr Tyr Leu Phe Ile Ser His Asp Leu Ala Val Val  
 525 530 535  
 Arg Ser Phe Cys Thr Glu Val Phe Ile Met Tyr Lys Gly Gln Ile Val  
 540 545 550 555  
 Glu Lys Gly Asn Thr Lys Arg Ile Phe Ser Asp Pro Gln His Pro Tyr  
 560 565 570  
 Thr Arg Met Leu Leu Asn Ala Gln Leu Pro Glu Thr Pro Asp Gln Arg  
 575 585 585  
 50 Gln

&lt;210&gt; 37

&lt;211&gt; 698

&lt;212&gt; PRT

&lt;213&gt; Chlamydia pneumoniae .

&lt;400&gt; 37

60 Met Pro Gly Ile Glu Lys Ala Ala Thr Thr Val Ala Val Pro Gln Asp  
 1 5 10 15

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	Lys	Ser	Glu	Glu	Glu	Lys	Val	Lys	Glu	Arg	Leu	Thr	Lys	Arg	Glu	Leu	
				20					25					30			
	Thr	Cys	Glu	Asp	Leu	Lys	Asp	Asn	Gly	Tyr	Thr	Val	Asn	Phe	Glu	Asp	
			35					40					45				
10	Ile	Ser	Ile	Leu	Glu	Leu	Leu	Gln	Phe	Val	Ser	Lys	Ile	Ser	Gly	Thr	
		50					55					60					
	Asn	Phe	Val	Phe	Asp	Ser	Asn	Asp	Leu	Gln	Phe	Asn	Val	Thr	Ile	Val	
	65					70				75						80	
	Ser	His	Asp	Pro	Thr	Ser	Val	Asp	Asp	Leu	Ser	Thr	Ile	Leu	Leu	Gln	
					85					90					95		
	Val	Leu	Lys	Met	His	Asp	Leu	Lys	Val	Val	Glu	Gln	Gly	Asn	Asn	Val	
				100					105					110			
20	Leu	Ile	Tyr	Arg	Asn	Pro	His	Leu	Ser	Lys	Leu	Ser	Thr	Val	Val	Thr	
			115					120					125				
	Asp	Ser	Ser	Leu	Lys	Glu	Thr	Cys	Glu	Ala	Val	Val	Val	Thr	Arg	Val	
		130					135						140				
	Phe	Arg	Leu	Tyr	Arg	Arg	Gln	Pro	Ser	Ala	Ala	Val	Asn	Ile	Ile	Gln	
	145					150					155					160	
30	Pro	Leu	Leu	Ser	His	Asp	Ala	Ile	Val	Ser	Ala	Ser	Glu	Ala	Thr	Arg	
					165					170					175		
	His	Val	Ile	Ile	Ser	Asp	Ile	Ala	Gly	Asn	Val	Asp	Lys	Val	Ser	Asp	
				180					185					190			
	Leu	Leu	Ala	Ala	Leu	Asp	Cys	Pro	Gly	Thr	Ser	Val	Asp	Met	Thr	Glu	
			195					200					205				
40	Tyr	Glu	Val	Lys	Tyr	Ala	Asn	Pro	Ala	Ala	Leu	Val	Ser	Tyr	Cys	Gln	
		210					215					220					
	Asp	Val	Leu	Gly	Thr	Leu	Ala	Glu	Asp	Asp	Ala	Phe	Gln	Met	Phe	Ile	
	225					230					235					240	
	Gln	Pro	Gly	Thr	Asn	Lys	Ile	Phe	Val	Val	Ser	Ser	Pro	Arg	Leu	Ala	
					245					250					255		
	Asn	Lys	Ala	Glu	Gln	Leu	Leu	Lys	Ser	Leu	Asp	Val	Pro	Glu	Met	Ala	
				260					265					270			
50	His	Thr	Leu	Asp	Asp	Pro	Ala	Ser	Thr	Ala	Leu	Ala	Leu	Gly	Gly	Thr	
			275					280						285			
	Gly	Thr	Thr	Ser	Pro	Lys	Ser	Leu	Arg	Phe	Phe	Met	Tyr	Lys	Leu	Lys	
		290					295					300					
	Tyr	Gln	Asn	Gly	Glu	Val	Ile	Ala	Asn	Ala	Leu	Gln	Asp	Ile	Gly	Tyr	
	305					310					315					320	
60	Asn	Leu	Tyr	Val	Thr	Thr	Ala	Met	Asp	Glu	Asp	Phe	Ile	Asn	Thr	Leu	
					325					330					335		

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	Asn	Ser	Ile	Gln	Trp	Leu	Glu	Val	Asn	Asn	Ser	Ile	Val	Ile	Ile	Gly	
				340					345					350			
	Asn	Gln	Gly	Asn	Val	Asp	Arg	Val	Ile	Gly	Leu	Leu	Asn	Gly	Leu	Asp	
			355					360					365				
10	Leu	Pro	Pro	Lys	Gln	Val	Tyr	Ile	Glu	Val	Leu	Ile	Leu	Asp	Thr	Ser	
		370					375					380					
	Leu	Glu	Lys	Ser	Trp	Asp	Phe	Gly	Val	Gln	Trp	Val	Ala	Leu	Gly	Asp	
	385					390					395				400		
	Glu	Gln	Ser	Lys	Val	Ala	Tyr	Ala	Ser	Gly	Leu	Leu	Asn	Asn	Thr	Gly	
					405					410					415		
	Ile	Ala	Thr	Pro	Thr	Lys	Ala	Thr	Val	Pro	Pro	Gly	Thr	Pro	Asn	Pro	
				420					425					430			
20	Gly	Ser	Ile	Pro	Leu	Pro	Thr	Pro	Gly	Gln	Leu	Thr	Gly	Phe	Ser	Asp	
			435					440					445				
	Met	Leu	Asn	Ser	Ser	Ser	Ala	Phe	Gly	Leu	Gly	Ile	Ile	Gly	Asn	Val	
	450						455					460					
	Leu	Ser	His	Lys	Gly	Lys	Ser	Phe	Leu	Thr	Leu	Gly	Gly	Leu	Leu	Ser	
	465					470					475					480	
30	Ala	Leu	Asp	Gln	Asp	Gly	Asp	Thr	Val	Ile	Val	Leu	Asn	Pro	Arg	Ile	
					485					490					495		
	Met	Ala	Gln	Asp	Thr	Gln	Gln	Ala	Ser	Phe	Phe	Val	Gly	Gln	Thr	Val	
				500					505					510			
	Pro	Tyr	Gln	Thr	Ile	Lys	Tyr	Tyr	Ile	Gln	Glu	Thr	Gly	Thr	Val	Thr	
			515					520					525				
40	Gln	Asn	Ile	Asp	Tyr	Glu	Asp	Ile	Gly	Val	Asn	Leu	Val	Val	Thr	Ser	
	530						535					540					
	Thr	Val	Ala	Pro	Asn	Asn	Val	Val	Thr	Leu	Gln	Ile	Glu	Gln	Thr	Ile	
	545					550					555					560	
	Ser	Glu	Leu	His	Ser	Ala	Ser	Gly	Ser	Leu	Thr	Pro	Val	Thr	Asp	Lys	
					565					570					575		
	Thr	Tyr	Ala	Ala	Thr	Arg	Leu	Gln	Ile	Pro	Asp	Gly	Cys	Phe	Leu	Val	
				580					585					590			
50	Met	Ser	Gly	His	Ile	Arg	Asp	Lys	Thr	Thr	Lys	Val	Val	Ser	Gly	Val	
			595					600					605				
	Pro	Leu	Leu	Asn	Ser	Ile	Pro	Leu	Ile	Arg	Gly	Leu	Phe	Ser	Arg	Thr	
		610					615					620					
	Ile	Asp	Gln	Arg	Gln	Lys	Arg	Asn	Ile	Met	Met	Phe	Ile	Lys	Pro	Lys	
	625					630				635					640		
60	Val	Ile	Ser	Ser	Phe	Glu	Glu	Gly	Thr	Arg	Val	Thr	Asn	Lys	Glu	Gly	
					645					650					655		

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Tyr Arg Tyr Asn Trp Glu Ala Asp Glu Gly Ser Met Gln Val Ala Pro  
 660 665 670

Arg His Ala Pro Glu Cys Gln Gly Pro Pro Ser Leu Gln Ala Glu Ser  
 675 680 685

10 Asp Phe Lys Ile Ile Glu Ile Glu Ala Gln  
 690 695

<210> 38

<211> 547

<212> PRT

<213> Chlamydia pneumoniae

<400> 38

20 Met Ser Arg Lys Asp Asn Glu Val Ser Leu Ala Arg Ser Ile Phe Asn  
 1 5 10 15

Ile Leu Ser Gly Thr Phe Cys Ser Arg Ile Thr Gly Ile Phe Arg Glu  
 20 25 30

Ile Ala Met Ala Thr Tyr Phe Gly Ala Asp Pro Ile Val Ala Ala Phe  
 35 40 45

30 Trp Leu Gly Phe Arg Thr Val Phe Phe Leu Arg Lys Ile Leu Gly Gly  
 50 55 60

Leu Ile Leu Glu Gln Ala Phe Ile Pro His Phe Glu Phe Leu Arg Ala  
 65 70 75 80

Gln Ser Leu Asp Arg Ala Ala Phe Phe Phe Arg Arg Phe Ser Arg Leu  
 85 90 95

Ile Lys Gly Ser Thr Ile Ile Phe Thr Leu Leu Ile Glu Ala Val Leu  
 100 105 110

40 Trp Val Phe Phe Asn Asn Val Glu Glu Gly Thr Tyr Asp Met Ile Leu  
 115 120 125

Leu Thr Met Ile Leu Leu Pro Cys Gly Ile Phe Leu Met Met Tyr Asn  
 130 135 140

Val Asn Gly Ala Leu Leu His Cys Gly Asn Lys Phe Phe Gly Val Gly  
 145 150 155 160

50 Leu Ala Pro Val Val Val Asn Ile Ile Trp Ile Phe Phe Val Ile Ala  
 165 170 175

Ala Arg His Ser Asp Pro Arg Glu Arg Ile Ile Gly Leu Ser Val Ala  
 180 185 190

Leu Val Ile Gly Phe Phe Phe Glu Trp Leu Ile Thr Val Pro Gly Val  
 195 200 205

Trp Lys Phe Leu Leu Glu Ala Lys Ser Pro Pro Gln Glu His Asp Ser  
 210 215 220

60

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	Val	Arg	Ala	Leu	Leu	Ala	Pro	Leu	Ser	Leu	Gly	Ile	Leu	Thr	Ser	Ser	
	225					230					235					240	
	Ile	Phe	Gln	Leu	Asn	Leu	Leu	Ser	Asp	Ile	Cys	Leu	Ala	Arg	Tyr	Val	
					245					250					255		
10	His	Glu	Ile	Gly	Pro	Leu	Tyr	Leu	Met	Tyr	Ser	Leu	Lys	Ile	Tyr	Gln	
				260					265					270			
	Leu	Pro	Ile	His	Leu	Phe	Gly	Phe	Gly	Val	Phe	Thr	Val	Leu	Leu	Pro	
			275					280					285				
	Ala	Ile	Ser	Arg	Cys	Val	Gln	Arg	Glu	Asp	His	Glu	Arg	Gly	Leu	Lys	
		290					295					300					
	Leu	Met	Lys	Phe	Val	Leu	Thr	Leu	Thr	Met	Ser	Val	Met	Ile	Ile	Met	
	305					310					315					320	
20	Thr	Ala	Gly	Leu	Leu	Leu	Leu	Ala	Leu	Pro	Gly	Val	Arg	Val	Leu	Tyr	
					325					330					335		
	Glu	His	Gly	Leu	Phe	Pro	Gln	Ser	Ala	Val	Tyr	Ala	Ile	Val	Arg	Val	
				340					345					350			
	Leu	Arg	Gly	Tyr	Gly	Ala	Ser	Ile	Ile	Pro	Met	Ala	Leu	Ala	Pro	Leu	
			355					360					365				
30	Val	Ser	Val	Leu	Phe	Tyr	Ala	Gln	Arg	Gln	Tyr	Ala	Val	Pro	Leu	Phe	
		370					375					380					
	Ile	Gly	Ile	Gly	Thr	Ala	Leu	Ala	Asn	Ile	Val	Leu	Ser	Leu	Val	Leu	
	385					390					395					400	
	Gly	Arg	Trp	Val	Leu	Lys	Asp	Val	Ser	Gly	Ile	Ser	Tyr	Ala	Thr	Ser	
				405						410					415		
40	Ile	Thr	Ala	Trp	Val	Gln	Leu	Tyr	Phe	Leu	Trp	Tyr	Tyr	Ser	Ser	Lys	
				420					425					430			
	Arg	Leu	Pro	Met	Tyr	Ser	Lys	Leu	Leu	Trp	Glu	Ser	Ile	Arg	Arg	Ser	
			435					440					445				
	Ile	Lys	Val	Met	Gly	Thr	Thr	Met	Leu	Ala	Cys	Met	Ile	Thr	Leu	Gly	
		450					455					460					
	Leu	Asn	Ile	Leu	Thr	Gln	Thr	Thr	Tyr	Val	Ile	Phe	Leu	Asn	Pro	Leu	
	465					470					475					480	
50	Thr	Pro	Leu	Ala	Trp	Pro	Leu	Ser	Ser	Ile	Thr	Ala	Gln	Ala	Ile	Ala	
					485					490					495		
	Phe	Leu	Ser	Glu	Ser	Cys	Ile	Phe	Leu	Ala	Phe	Leu	Phe	Gly	Phe	Ala	
				500					505					510			
	Lys	Leu	Leu	Arg	Val	Glu	Asp	Leu	Ile	Asn	Leu	Ala	Ser	Phe	Glu	Tyr	
			515					520					525				
60	Trp	Arg	Gly	Gln	Arg	Gly	Leu	Leu	Gln	Arg	Gln	His	Val	Met	Gln	Asp	
		530					535					540					

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Thr Gln Asn  
545

<210> 39  
<211> 535  
<212> PRT

10 <213> Chlamydia pneumoniae

<400> 39

Arg Lys Asp Asn Glu Val Ser Leu Ala Arg Ser Ile Phe Asn  
1 5 10

Ile Leu Ser Gly Thr Phe Cys Ser Arg Ile Thr Gly Ile Phe Arg Glu  
15 20 25 30

20 Ile Ala Met Ala Thr Tyr Phe Gly Ala Asp Pro Ile Val Ala Ala Phe  
35 40 45

Trp Leu Gly Phe Arg Thr Val Phe Phe Leu Arg Lys Ile Leu Gly Gly  
50 55 60

Leu Ile Leu Glu Gln Ala Phe Ile Pro His Phe Glu Phe Leu Arg Ala  
65 70 75

30 Gln Ser Leu Asp Arg Ala Ala Phe Phe Phe Arg Arg Phe Ser Arg Leu  
80 85 90

Ile Lys Gly Ser Thr Ile Ile Phe Thr Leu Leu Ile Glu Ala Val Leu  
95 100 105 110

Trp Val Phe Phe Asn Asn Val Glu Glu Gly Thr Tyr Asp Met Ile Leu  
115 120 125

Leu Thr Met Ile Leu Leu Pro Cys Gly Ile Phe Leu Met Met Tyr Asn  
130 135 140

40 Val Asn Gly Ala Leu Leu His Cys Gly Asn Lys Phe Phe Gly Val Gly  
145 150 155

Leu Ala Pro Val Val Val Asn Ile Ile Trp Ile Phe Phe Val Ile Ala  
160 165 170

Ala Arg His Ser Asp Pro Arg Glu Arg Ile Ile Gly Leu Ser Val Ala  
175 180 185 190

50 Leu Val Ile Gly Phe Phe Phe Glu Trp Leu Ile Thr Val Pro Gly Val  
195 200 205

Trp Lys Phe Leu Leu Glu Ala Lys Ser Pro Pro Gln Glu His Asp Ser  
210 215 220

Val Arg Ala Leu Leu Ala Pro Leu Ser Leu Gly Ile Leu Thr Ser Ser  
225 230 235

Ile Phe Gln Leu Asn Leu Leu Ser Asp Ile Cys Leu Ala Arg Tyr Val  
240 245 250

60



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His Glu Ile Gly Pro Leu Tyr Leu Met Tyr Ser Leu Lys Ile Tyr Gln  
 255 260 265 270  
 Leu Pro Ile His Leu Phe Gly Phe Gly Val Phe Thr Val Leu Leu Pro  
 275 280 285  
 10 Ala Ile Ser Arg Cys Val Gln Arg Glu Asp His Glu Arg Gly Leu Lys  
 290 295 300  
 Leu Met Lys Phe Val Leu Thr Leu Thr Met Ser Val Met Ile Ile Met  
 305 310 315  
 Thr Ala Gly Leu Leu Leu Leu Ala Leu Pro Gly Val Arg Val Leu Tyr  
 320 325 330  
 Glu His Gly Leu Phe Pro Gln Ser Ala Val Tyr Ala Ile Val Arg Val  
 335 340 345 350  
 20 Leu Arg Gly Tyr Gly Ala Ser Ile Ile Pro Met Ala Leu Ala Pro Leu  
 355 360 365  
 Val Ser Val Leu Phe Tyr Ala Gln Arg Gln Tyr Ala Val Pro Leu Phe  
 370 375 380  
 Ile Gly Ile Gly Thr Ala Leu Ala Asn Ile Val Leu Ser Leu Val Leu  
 385 390 395  
 30 Gly Arg Trp Val Leu Lys Asp Val Ser Gly Ile Ser Tyr Ala Thr Ser  
 400 405 410  
 Ile Thr Ala Trp Val Gln Leu Tyr Phe Leu Trp Tyr Tyr Ser Ser Lys  
 415 420 425 430  
 Arg Leu Pro Met Tyr Ser Lys Leu Leu Trp Glu Ser Ile Arg Arg Ser  
 435 440 445  
 40 Ile Lys Val Met Gly Thr Thr Met Leu Ala Cys Met Ile Thr Leu Gly  
 450 455 460  
 Leu Asn Ile Leu Thr Gln Thr Thr Tyr Val Ile Phe Leu Asn Pro Leu  
 465 470 475  
 Thr Pro Leu Ala Trp Pro Leu Ser Ser Ile Thr Ala Gln Ala Ile Ala  
 480 485 490  
 Phe Leu Ser Glu Ser Cys Ile Phe Leu Ala Phe Leu Phe Gly Phe Ala  
 495 500 505 510  
 50 Lys Leu Leu Arg Val Glu Asp Leu Ile Asn Leu Ala Ser Phe Glu Tyr  
 515 520 525  
 Trp Arg Gly Gln Arg Gly Leu Leu Gln  
 530 535

&lt;210&gt; 40

&lt;211&gt; 954

60 &lt;212&gt; PRT

&lt;213&gt; Chlamydia pneumoniae

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&lt;400&gt; 40

	Met	Lys	Thr	Ser	Arg	Asn	Lys	Gln	Cys	Lys	Ile	Thr	Asp	Pro	Leu	Ser
	1				5					10					15	
	Lys	Ser	Ser	Phe	Phe	Val	Gly	Ala	Leu	Ile	Leu	Gly	Lys	Thr	Thr	Ile
				20					25					30		
10	Leu	Leu	Asn	Ala	Thr	Pro	Leu	Ser	Asp	Tyr	Phe	Asp	Asn	Gln	Ala	Asn
			35					40					45			
	Gln	Leu	Thr	Thr	Leu	Phe	Pro	Leu	Ile	Asp	Thr	Leu	Thr	Asn	Met	Thr
		50					55					60				
	Pro	Tyr	Ser	His	Arg	Ala	Thr	Leu	Phe	Gly	Val	Arg	Asp	Asp	Thr	Asn
	65					70					75					80
20	Gln	Asp	Ile	Val	Leu	Asp	His	Gln	Asn	Ser	Ile	Glu	Ser	Trp	Phe	Glu
					85					90					95	
	Asn	Phe	Ser	Gln	Asp	Gly	Gly	Ala	Leu	Ser	Cys	Lys	Ser	Leu	Ala	Ile
				100					105					110		
	Thr	Asn	Thr	Lys	Asn	Gln	Ile	Leu	Phe	Leu	Asn	Ser	Phe	Ala	Ile	Lys
				115				120						125		
30	Arg	Ala	Gly	Ala	Met	Tyr	Val	Asp	Gly	Asn	Phe	Asp	Leu	Ser	Glu	Asn
		130					135					140				
	His	Gly	Ser	Ile	Ile	Phe	Ser	Gly	Asn	Leu	Ser	Phe	Pro	Asn	Ala	Ser
	145					150					155					160
	Asn	Phe	Ala	Asp	Thr	Cys	Thr	Gly	Gly	Ala	Val	Leu	Cys	Ser	Lys	Asn
					165					170					175	
	Val	Thr	Ile	Ser	Lys	Asn	Gln	Gly	Thr	Ala	Tyr	Phe	Ile	Asn	Asn	Lys
				180					185					190		
40	Ala	Lys	Ser	Ser	Gly	Gly	Ala	Ile	Gln	Ala	Ala	Ile	Ile	Asn	Ile	Lys
			195					200					205			
	Asp	Asn	Thr	Gly	Pro	Cys	Leu	Phe	Phe	Asn	Asn	Ala	Ala	Gly	Gly	Thr
		210					215					220				
	Ala	Gly	Gly	Ala	Leu	Phe	Ala	Asn	Ala	Cys	Arg	Ile	Glu	Asn	Asn	Ser
	225					230					235					240
50	Gln	Pro	Ile	Tyr	Phe	Leu	Asn	Asn	Gln	Ser	Gly	Leu	Gly	Gly	Ala	Ile
					245					250					255	
	Arg	Val	His	Gln	Glu	Cys	Ile	Leu	Thr	Lys	Asn	Thr	Gly	Ser	Val	Ile
				260					265					270		
	Phe	Asn	Asn	Asn	Phe	Ala	Met	Glu	Ala	Asp	Ile	Ser	Ala	Asn	His	Ser
				275				280					285			
60	Ser	Gly	Gly	Ala	Ile	Tyr	Cys	Ile	Ser	Cys	Ser	Ile	Lys	Asp	Asn	Pro
		290					295					300				

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	Gly	Ile	Ala	Ala	Phe	Asp	Asn	Asn	Thr	Ala	Ala	Arg	Asp	Gly	Gly	Ala	
	305					310					315					320	
	Ile	Cys	Thr	Gln	Ser	Leu	Thr	Ile	Gln	Asp	Ser	Gly	Pro	Val	Tyr	Phe	
					325					330						335	
10	Thr	Asn	Asn	Gln	Gly	Thr	Trp	Gly	Gly	Ala	Ile	Met	Leu	Arg	Gln	Asp	
				340					345						350		
	Gly	Ala	Cys	Thr	Leu	Phe	Ala	Asp	Gln	Gly	Asp	Ile	Ile	Phe	Tyr	Asn	
			355					360						365			
	Asn	Arg	His	Phe	Lys	Asp	Thr	Phe	Ser	Asn	His	Val	Ser	Val	Asn	Cys	
							375					380					
	Thr	Arg	Asn	Val	Ser	Leu	Thr	Val	Gly	Ala	Ser	Gln	Gly	His	Ser	Ala	
	385					390					395					400	
20	Thr	Phe	Tyr	Asp	Pro	Ile	Leu	Gln	Arg	Tyr	Thr	Ile	Gln	Asn	Ser	Ile	
					405					410					415		
	Gln	Lys	Phe	Asn	Pro	Asn	Pro	Glu	His	Leu	Gly	Thr	Ile	Leu	Phe	Ser	
				420					425						430		
	Ser	Thr	Tyr	Ile	Pro	Asp	Thr	Ser	Thr	Ser	Arg	Asp	Asp	Phe	Ile	Ser	
			435					440					445				
30	His	Phe	Arg	Asn	His	Ile	Gly	Leu	Tyr	Asn	Gly	Thr	Leu	Ala	Leu	Glu	
		450					455					460					
	Asp	Arg	Ala	Glu	Trp	Lys	Val	Tyr	Lys	Phe	Asp	Gln	Phe	Gly	Gly	Thr	
	465					470					475					480	
	Leu	Arg	Leu	Gly	Ser	Arg	Ala	Val	Phe	Ser	Thr	Thr	Asp	Glu	Glu	Gln	
					485					490					495		
40	Ser	Ser	Ser	Ser	Val	Gly	Ser	Val	Ile	Asn	Ile	Asn	Asn	Leu	Ala	Ile	
					500				505						510		
	Asn	Leu	Pro	Ser	Ile	Leu	Gly	Asn	Arg	Val	Ala	Pro	Lys	Leu	Trp	Ile	
			515					520					525				
	Arg	Pro	Thr	Gly	Ser	Ser	Ala	Pro	Tyr	Ser	Glu	Asp	Asn	Asn	Pro	Ile	
		530					535					540					
	Ile	Asn	Leu	Ser	Gly	Pro	Leu	Ser	Leu	Leu	Asp	Asp	Glu	Asn	Leu	Asp	
	545					550					555					560	
50	Pro	Tyr	Asp	Thr	Ala	Asp	Leu	Ala	Gln	Pro	Ile	Ala	Glu	Val	Pro	Leu	
					565					570					575		
	Leu	Tyr	Leu	Leu	Asp	Val	Thr	Ala	Lys	His	Ile	Asn	Thr	Asp	Asn	Phe	
					580				585					590			
	Tyr	Pro	Glu	Gly	Leu	Asn	Thr	Thr	Gln	His	Tyr	Gly	Tyr	Gln	Gly	Val	
			595				600						605				
60	Trp	Ser	Pro	Tyr	Trp	Ile	Glu	Thr	Ile	Thr	Thr	Ser	Asp	Thr	Ser	Ser	
		610					615					620					

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	Glu	Asp	Thr	Val	Asn	Thr	Leu	His	Arg	Gln	Leu	Tyr	Gly	Asp	Trp	Thr	
	625					630					635					640	
	Pro	Thr	Gly	Tyr	Lys	Val	Asn	Pro	Glu	Asn	Lys	Gly	Asp	Ile	Ala	Leu	
					645					650					655		
10	Ser	Ala	Phe	Trp	Gln	Ser	Phe	His	Asn	Leu	Phe	Ala	Thr	Leu	Arg	Tyr	
				660					665					670			
	Gln	Thr	Gln	Gln	Gly	Gln	Ile	Ala	Pro	Thr	Ala	Ser	Gly	Glu	Ala	Thr	
			675					680					685				
	Arg	Leu	Phe	Val	His	Gln	Asn	Ser	Asn	Asn	Asp	Ala	Lys	Gly	Phe	His	
	690						695					700					
	Met	Glu	Ala	Thr	Gly	Tyr	Ser	Leu	Gly	Thr	Thr	Ser	Asn	Thr	Ala	Ser	
	705					710					715					720	
20	Asn	His	Ser	Phe	Gly	Val	Asn	Phe	Ser	Gln	Leu	Phe	Ser	Asn	Leu	Tyr	
					725					730					735		
	Glu	Ser	His	Ser	Asp	Asn	Ser	Val	Ala	Ser	His	Thr	Thr	Thr	Val	Ala	
				740					745						750		
	Leu	Gln	Ile	Asn	Asn	Pro	Trp	Leu	Gln	Glu	Arg	Phe	Ser	Thr	Ser	Ala	
			755					760					765				
30	Ser	Leu	Ala	Tyr	Ser	Tyr	Ser	Asn	His	His	Ile	Lys	Ala	Ser	Gly	Tyr	
		770					775					780					
	Ser	Gly	Lys	Ile	Gln	Thr	Glu	Gly	Lys	Cys	Tyr	Ser	Thr	Thr	Leu	Gly	
	785					790					795				800		
	Ala	Ala	Leu	Ser	Cys	Ser	Leu	Ser	Leu	Gln	Trp	Arg	Ser	Arg	Pro	Leu	
					805					810					815		
40	His	Phe	Thr	Pro	Phe	Ile	Gln	Ala	Ile	Ala	Val	Arg	Ser	Asn	Gln	Thr	
				820					825					830			
	Ala	Phe	Gln	Glu	Ser	Gly	Asp	Lys	Ala	Arg	Lys	Phe	Ser	Val	His	Lys	
			835					840					845				
	Pro	Leu	Tyr	Asn	Leu	Thr	Val	Pro	Leu	Gly	Ile	Gln	Ser	Ala	Trp	Glu	
		850					855					860					
	Ser	Lys	Phe	Arg	Leu	Pro	Thr	Tyr	Trp	Asn	Ile	Glu	Leu	Ala	Tyr	Gln	
	865					870					875					880	
50	Pro	Val	Leu	Tyr	Gln	Gln	Asn	Pro	Glu	Ile	Asn	Val	Ser	Leu	Glu	Ser	
					885					890					895		
	Ser	Gly	Ser	Ser	Trp	Leu	Leu	Ser	Gly	Thr	Thr	Leu	Ala	Arg	Asn	Ala	
				900					905					910			
	Ile	Ala	Phe	Lys	Gly	Arg	Asn	Gln	Ile	Phe	Ile	Phe	Pro	Lys	Leu	Ser	
			915					920					925				
60	Val	Phe	Leu	Asp	Tyr	Gln	Gly	Ser	Val	Ser	Ser	Ser	Thr	Thr	Thr	His	
		930					935					940					

69/83

Tyr Leu His Ala Gly Thr Thr Phe Lys Phe  
945 950

<210> 41  
<211> 788  
<212> PRT

10 <213> Chlamydia pneumoniae

<400> 41

Thr Gly Gly Ala Val Leu Cys Ser Lys Asn  
1 5 10

Val Thr Ile Ser Lys Asn Gln Gly Thr Ala Tyr Phe Ile Asn Asn Lys  
15 20 25

20 Ala Lys Ser Ser Gly Gly Ala Ile Gln Ala Ala Ile Ile Asn Ile Lys  
30 35 40

Asp Asn Thr Gly Pro Cys Leu Phe Phe Asn Asn Ala Ala Gly Gly Thr  
45 50 55

Ala Gly Gly Ala Leu Phe Ala Asn Ala Cys Arg Ile Glu Asn Asn Ser  
60 65 70

30 Gln Pro Ile Tyr Phe Leu Asn Asn Gln Ser Gly Leu Gly Gly Ala Ile  
75 80 85 90

Arg Val His Gln Glu Cys Ile Leu Thr Lys Asn Thr Gly Ser Val Ile  
95 100 105

Phe Asn Asn Asn Phe Ala Met Glu Ala Asp Ile Ser Ala Asn His Ser  
110 115 120

Ser Gly Gly Ala Ile Tyr Cys Ile Ser Cys Ser Ile Lys Asp Asn Pro  
125 130 135

40 Gly Ile Ala Ala Phe Asp Asn Asn Thr Ala Ala Arg Asp Gly Gly Ala  
140 145 150

Ile Cys Thr Gln Ser Leu Thr Ile Gln Asp Ser Gly Pro Val Tyr Phe  
155 160 165 170

Thr Asn Asn Gln Gly Thr Trp Gly Gly Ala Ile Met Leu Arg Gln Asp  
175 180 185

50 Gly Ala Cys Thr Leu Phe Ala Asp Gln Gly Asp Ile Ile Phe Tyr Asn  
190 195 200

Asn Arg His Phe Lys Asp Thr Phe Ser Asn His Val Ser Val Asn Cys  
205 210 215

Thr Arg Asn Val Ser Leu Thr Val Gly Ala Ser Gln Gly His Ser Ala  
220 225 230

Thr Phe Tyr Asp Pro Ile Leu Gln Arg Tyr Thr Ile Gln Asn Ser Ile  
235 240 245 250

60

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	Gln	Lys	Phe	Asn	Pro	Asn	Pro	Glu	His	Leu	Gly	Thr	Ile	Leu	Phe	Ser	
					255					260					265		
	Ser	Thr	Tyr	Ile	Pro	Asp	Thr	Ser	Thr	Ser	Arg	Asp	Asp	Phe	Ile	Ser	
				270					275					280			
10	His	Phe	Arg	Asn	His	Ile	Gly	Leu	Tyr	Asn	Gly	Thr	Leu	Ala	Leu	Glu	
			285					290					295				
	Asp	Arg	Ala	Glu	Trp	Lys	Val	Tyr	Lys	Phe	Asp	Gln	Phe	Gly	Gly	Thr	
		300					305					310					
	Leu	Arg	Leu	Gly	Ser	Arg	Ala	Val	Phe	Ser	Thr	Thr	Asp	Glu	Glu	Gln	
	315					320					325					330	
	Ser	Ser	Ser	Ser	Val	Gly	Ser	Val	Ile	Asn	Ile	Asn	Asn	Leu	Ala	Ile	
					335					340					345		
20	Asn	Leu	Pro	Ser	Ile	Leu	Gly	Asn	Arg	Val	Ala	Pro	Lys	Leu	Trp	Ile	
				350					355					360			
	Arg	Pro	Thr	Gly	Ser	Ser	Ala	Pro	Tyr	Ser	Glu	Asp	Asn	Asn	Pro	Ile	
			365					370					375				
	Ile	Asn	Leu	Ser	Gly	Pro	Leu	Ser	Leu	Leu	Asp	Asp	Glu	Asn	Leu	Asp	
		380					385					390					
30	Pro	Tyr	Asp	Thr	Ala	Asp	Leu	Ala	Gln	Pro	Ile	Ala	Glu	Val	Pro	Leu	
	395					400					405					410	
	Leu	Tyr	Leu	Leu	Asp	Val	Thr	Ala	Lys	His	Ile	Asn	Thr	Asp	Asn	Phe	
					415					420					425		
	Tyr	Pro	Glu	Gly	Leu	Asn	Thr	Thr	Gln	His	Tyr	Gly	Tyr	Gln	Gly	Val	
				430					435					440			
	Trp	Ser	Pro	Tyr	Trp	Ile	Glu	Thr	Ile	Thr	Thr	Ser	Asp	Thr	Ser	Ser	
40			445					450					455				
	Glu	Asp	Thr	Val	Asn	Thr	Leu	His	Arg	Gln	Leu	Tyr	Gly	Asp	Trp	Thr	
	460						465					470					
	Pro	Thr	Gly	Tyr	Lys	Val	Asn	Pro	Glu	Asn	Lys	Gly	Asp	Ile	Ala	Leu	
	475					480					485					490	
	Ser	Ala	Phe	Trp	Gln	Ser	Phe	His	Asn	Leu	Phe	Ala	Thr	Leu	Arg	Tyr	
					495					500					505		
50	Gln	Thr	Gln	Gln	Gly	Gln	Ile	Ala	Pro	Thr	Ala	Ser	Gly	Glu	Ala	Thr	
				510					515					520			
	Arg	Leu	Phe	Val	His	Gln	Asn	Ser	Asn	Asn	Asp	Ala	Lys	Gly	Phe	His	
			525					530					535				
	Met	Glu	Ala	Thr	Gly	Tyr	Ser	Leu	Gly	Thr	Thr	Ser	Asn	Thr	Ala	Ser	
		540					545					550					
60	Asn	His	Ser	Phe	Gly	Val	Asn	Phe	Ser	Gln	Leu	Phe	Ser	Asn	Leu	Tyr	
	555					560					565					570	

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Glu Ser His Ser Asp Asn Ser Val Ala Ser His Thr Thr Thr Val Ala  
575 580 585

Leu Gln Ile Asn Asn Pro Trp Leu Gln Glu Arg Phe Ser Thr Ser Ala  
590 595 600

10      Ser Leu Ala Tyr Ser Tyr Ser Asn His His Ile Lys Ala Ser Gly Tyr  
              605                        610                        615

Ser Gly Lys Ile Gln Thr Glu Gly Lys Cys Tyr Ser Thr Thr Leu Gly  
620 625 630

Ala Ala Leu Ser Cys Ser Leu Ser Leu Gln Trp Arg Ser Arg Pro Leu  
635 640 645 650

His Phe Thr Pro Phe Ile Gln Ala Ile Ala Val Arg Ser Asn Gln Thr  
655 660 665

Ala Phe Gln Glu Ser Gly Asp Lys Ala Arg Lys Phe Ser Val His Lys  
670 675 680

Pro Leu Tyr Asn Leu Thr Val Pro Leu Gly Ile Gln Ser Ala Trp Glu  
685 690 695

Ser Lys Phe Arg Leu Pro Thr Tyr Trp Asn Ile Glu Leu Ala Tyr Gln  
700 705 710

30    Pro Val Leu Tyr Gln Gln Asn Pro Glu Ile Asn Val Ser Leu Glu Ser  
       715                        720                        725                        730

Ser Gly Ser Ser Trp Leu Leu Ser Gly Thr Thr Leu Ala Arg Asn Ala  
735 740 745

Ile Ala Phe Lys Gly Arg Asn Gln Ile Phe Ile Phe Pro Lys Leu Ser  
750 755 760

Val Phe Leu Asp Tyr Gln Gly Ser Val Ser Ser Ser Thr Thr Thr His  
40 765 770 775

Tyr Leu His Ala Gly Thr Thr Phe Lys Phe  
780 785

<210> 42

<211> 1000

<212> PRT

<213> Chlamydia pneumoniae

50

<400> 42

Met Gln Val Phe Pro Lys Val Thr Leu Ser Leu Asp Tyr Ser Ala Asp  
1 5 10 15

Ile Ser Ser Ser Thr Leu Ser His Tyr Leu Asn Val Ala Ser Arg Met  
20 25 30

Arg Phe Leu Thr Ile Ser Asp Gln Asn Arg Lys Ile Lys Glu Pro Leu  
35 40 45

60

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	Val	Ser	Lys	Thr	Pro	Pro	Lys	Phe	Leu	Phe	Tyr	Leu	Gly	Asn	Phe	Thr	
	50						55					60					
	Ala	Cys	Met	Phe	Gly	Met	Thr	Pro	Ala	Val	Tyr	Ser	Leu	Gln	Thr	Asp	
	65					70					75					80	
10	Ser	Leu	Glu	Lys	Phe	Ala	Leu	Glu	Arg	Asp	Glu	Glu	Phe	Arg	Thr	Ser	
					85					90					95		
	Phe	Pro	Leu	Leu	Asp	Ser	Leu	Ser	Thr	Leu	Thr	Gly	Phe	Ser	Pro	Ile	
				100					105					110			
	Thr	Thr	Phe	Val	Gly	Asn	Arg	His	Asn	Ser	Ser	Gln	Asp	Ile	Val	Leu	
				115				120					125				
	Ser	Asn	Tyr	Lys	Ser	Ile	Asp	Asn	Ile	Leu	Leu	Leu	Trp	Thr	Ser	Ala	
		130					135					140					
20	Gly	Gly	Ala	Val	Ser	Cys	Asn	Asn	Phe	Leu	Leu	Ser	Asn	Val	Glu	Asp	
	145					150					155					160	
	His	Ala	Phe	Phe	Ser	Lys	Asn	Leu	Ala	Ile	Gly	Thr	Gly	Gly	Ala	Ile	
					165					170					175		
	Ala	Cys	Gln	Gly	Ala	Cys	Thr	Ile	Thr	Lys	Asn	Arg	Gly	Pro	Leu	Ile	
				180					185					190			
30	Phe	Phe	Ser	Asn	Arg	Gly	Leu	Asn	Asn	Ala	Ser	Thr	Gly	Gly	Glu	Thr	
			195					200					205				
	Arg	Gly	Gly	Ala	Ile	Ala	Cys	Asn	Gly	Asp	Phe	Thr	Ile	Ser	Gln	Asn	
		210					215					220					
	Gln	Gly	Thr	Phe	Tyr	Phe	Val	Asn	Asn	Ser	Val	Asn	Asn	Trp	Gly	Gly	
	225					230					235					240	
	Ala	Leu	Ser	Thr	Asn	Gly	His	Cys	Arg	Ile	Gln	Ser	Asn	Arg	Ala	Pro	
40					245					250					255		
	Leu	Leu	Phe	Phe	Asn	Asn	Thr	Ala	Pro	Ser	Gly	Gly	Gly	Ala	Leu	Arg	
				260					265					270			
	Ser	Glu	Asn	Thr	Thr	Ile	Ser	Asp	Asn	Thr	Arg	Pro	Ile	Tyr	Phe	Lys	
			275					280					285				
	Asn	Asn	Cys	Gly	Asn	Asn	Gly	Gly	Ala	Ile	Gln	Thr	Ser	Val	Thr	Val	
		290					295					300					
50	Ala	Ile	Lys	Asn	Asn	Ser	Gly	Ser	Val	Ile	Phe	Asn	Asn	Asn	Thr	Ala	
	305					310					315					320	
	Leu	Ser	Gly	Ser	Ile	Asn	Ser	Gly	Asn	Gly	Ser	Gly	Gly	Ala	Ile	Tyr	
					325					330					335		
	Thr	Thr	Asn	Leu	Ser	Ile	Asp	Asp	Asn	Pro	Gly	Thr	Ile	Leu	Phe	Asn	
				340					345					350			
60	Asn	Asn	Tyr	Cys	Ile	Arg	Asp	Gly	Gly	Ala	Ile	Cys	Thr	Gln	Phe	Leu	
			355					360					365				



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	Thr	Ile	Lys	Asn	Ser	Gly	His	Val	Tyr	Phe	Thr	Asn	Asn	Gln	Gly	Asn	
	370						375					380					
	Trp	Gly	Gly	Ala	Leu	Met	Leu	Leu	Gln	Asp	Ser	Thr	Cys	Leu	Leu	Phe	
	385					390					395					400	
10	Ala	Glu	Gln	Gly	Asn	Ile	Ala	Phe	Gln	Asn	Asn	Glu	Val	Phe	Leu	Thr	
					405					410					415		
	Thr	Phe	Gly	Arg	Tyr	Asn	Ala	Ile	His	Cys	Thr	Pro	Asn	Ser	Asn	Leu	
				420					425					430			
	Gln	Leu	Gly	Ala	Asn	Lys	Gly	Tyr	Thr	Thr	Ala	Phe	Phe	Asp	Pro	Ile	
			435					440					445				
20	Glu	His	Gln	His	Pro	Thr	Thr	Asn	Pro	Leu	Ile	Phe	Asn	Pro	Asn	Ala	
	450						455					460					
	Asn	His	Gln	Gly	Thr	Ile	Leu	Phe	Ser	Ser	Ala	Tyr	Ile	Pro	Glu	Ala	
	465					470					475					480	
	Ser	Asp	Tyr	Glu	Asn	Asn	Phe	Ile	Ser	Ser	Ser	Lys	Asn	Thr	Ser	Glu	
					485					490					495		
	Leu	Arg	Asn	Gly	Val	Leu	Ser	Ile	Glu	Asp	Arg	Ala	Gly	Trp	Gln	Phe	
				500					505					510			
30	Tyr	Lys	Phe	Thr	Gln	Lys	Gly	Gly	Ile	Leu	Lys	Leu	Gly	His	Ala	Ala	
			515					520					525				
	Ser	Ile	Ala	Thr	Thr	Ala	Asn	Ser	Glu	Thr	Pro	Ser	Thr	Ser	Val	Gly	
			530				535					540					
	Ser	Gln	Val	Ile	Ile	Asn	Asn	Leu	Ala	Ile	Asn	Leu	Pro	Ser	Ile	Leu	
	545					550					555					560	
40	Ala	Lys	Gly	Lys	Ala	Pro	Thr	Leu	Trp	Ile	Arg	Pro	Leu	Gln	Ser	Ser	
					565					570					575		
	Ala	Pro	Phe	Thr	Glu	Asp	Asn	Asn	Pro	Thr	Ile	Thr	Leu	Ser	Gly	Pro	
				580					585					590			
	Leu	Thr	Leu	Leu	Asn	Glu	Glu	Asn	Arg	Asp	Pro	Tyr	Asp	Ser	Ile	Asp	
			595					600					605				
50	Leu	Ser	Glu	Pro	Leu	Gln	Asn	Ile	His	Leu	Leu	Ser	Leu	Ser	Asp	Val	
	610						615					620					
	Thr	Ala	Arg	His	Ile	Asn	Thr	Asp	Asn	Phe	His	Pro	Glu	Ser	Leu	Asn	
	625					630					635					640	
	Ala	Thr	Glu	His	Tyr	Gly	Tyr	Gln	Gly	Ile	Trp	Ser	Pro	Tyr	Trp	Val	
					645					650					655		
	Glu	Thr	Ile	Thr	Thr	Asn	Asn	Ala	Ser	Ile	Glu	Thr	Ala	Asn	Thr		
				660				665					670				
60	Leu	Tyr	Arg	Ala	Leu	Tyr	Ala	Asn	Trp	Thr	Pro	Leu	Gly	Tyr	Lys	Val	
			675					680					685				

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	Asn	Pro	Glu	Tyr	Gln	Gly	Asp	Leu	Ala	Thr	Thr	Pro	Leu	Trp	Gln	Ser
	690						695					700				
	Phe	His	Thr	Met	Phe	Ser	Leu	Leu	Arg	Ser	Tyr	Asn	Arg	Thr	Gly	Asp
	705					710					715					720
10	Ser	Asp	Ile	Glu	Arg	Pro	Phe	Leu	Glu	Ile	Gln	Gly	Ile	Ala	Asp	Gly
					725					730					735	
	Leu	Phe	Val	His	Gln	Asn	Ser	Ile	Pro	Gly	Ala	Pro	Gly	Phe	Arg	Ile
				740					745					750		
	Gln	Ser	Thr	Gly	Tyr	Ser	Leu	Gln	Ala	Ser	Ser	Glu	Thr	Ser	Leu	His
				755				760					765			
	Gln	Lys	Ile	Ser	Leu	Gly	Phe	Ala	Gln	Phe	Phe	Thr	Arg	Thr	Lys	Glu
		770					775					780				
20	Ile	Gly	Ser	Ser	Asn	Asn	Val	Ser	Ala	His	Asn	Thr	Val	Ser	Ser	Leu
	785					790					795					800
	Tyr	Val	Glu	Leu	Pro	Trp	Phe	Gln	Glu	Ala	Phe	Ala	Thr	Ser	His	Ser
					805					810					815	
	Leu	Ala	Tyr	Gly	Tyr	Gly	Asp	His	His	Leu	His	Ala	Tyr	Ile	Arg	His
				820					825					830		
30	Ile	Lys	Asn	Arg	Ala	Glu	Gly	Thr	Cys	Tyr	Ser	His	Thr	Leu	Ala	Ala
			835					840					845			
	Ala	Ile	Gly	Cys	Ser	Phe	Pro	Trp	Gln	Gln	Lys	Ser	Tyr	Leu	His	Leu
		850					855					860				
	Ser	Pro	Phe	Val	Gln	Ala	Ile	Ala	Ile	Arg	Ser	His	Gln	Thr	Ala	Phe
	865					870					875					880
40	Glu	Glu	Ile	Gly	Asp	Asn	Pro	Arg	Lys	Phe	Val	Ser	Gln	Lys	Pro	Phe
					885					890					895	
	Tyr	Asn	Leu	Thr	Leu	Pro	Leu	Gly	Ile	Gln	Gly	Lys	Trp	Gln	Ser	Lys
				900					905					910		
	Phe	His	Val	Pro	Thr	Glu	Trp	Thr	Leu	Glu	Leu	Ser	Tyr	Gln	Pro	Val
			915					920					925			
	Leu	Tyr	Gln	Gln	Asn	Pro	Gln	Ile	Gly	Val	Thr	Leu	Leu	Ala	Ser	Gly
		930					935					940				
50	Gly	Ser	Trp	Asp	Ile	Leu	Gly	His	Asn	Tyr	Val	Arg	Asn	Ala	Leu	Gly
	945					950					955					960
	Tyr	Lys	Val	His	Asn	Gln	Thr	Ala	Leu	Phe	Arg	Ser	Leu	Asp	Leu	Phe
					965					970					975	
	Leu	Asp	Tyr	Gln	Gly	Ser	Val	Ser	Ser	Ser	Thr	Ser	Thr	His	His	Leu
				980					985					990		
60	Gln	Ala	Gly	Ser	Thr	Leu	Lys	Phe								
			995					1000								

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<210> 43  
 <211> 931  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 43

10	Met	Leu	Leu	Pro	Phe	Thr	Phe	Val	Leu	Ala	Asn	Glu	Gly	Leu	Gln	Leu	1	5	10	15
	Pro	Leu	Glu	Thr	Tyr	Ile	Thr	Leu	Ser	Pro	Glu	Tyr	Gln	Ala	Ala	Pro	20	25	30	
	Gln	Val	Gly	Phe	Thr	His	Asn	Gln	Asn	Gln	Asp	Leu	Ala	Ile	Val	Gly	35	40	45	
	Asn	His	Asn	Asp	Phe	Ile	Leu	Asp	Tyr	Lys	Tyr	Tyr	Arg	Ser	Asn	Gly	50	55	60	
20	Gly	Ala	Leu	Thr	Cys	Lys	Asn	Leu	Leu	Ile	Ser	Glu	Asn	Ile	Gly	Asn	65	70	75	80
	Val	Phe	Phe	Glu	Lys	Asn	Val	Cys	Pro	Asn	Ser	Gly	Gly	Ala	Ile	Tyr	85	90	95	
	Ala	Ala	Gln	Asn	Cys	Thr	Ile	Ser	Lys	Asn	Gln	Asn	Tyr	Ala	Phe	Thr	100	105	110	
30	Thr	Asn	Leu	Val	Ser	Asp	Asn	Pro	Thr	Ala	Thr	Ala	Gly	Ser	Leu	Leu	115	120	125	
	Gly	Gly	Ala	Leu	Phe	Ala	Ile	Asn	Cys	Ser	Ile	Thr	Asn	Asn	Leu	Gly	130	135	140	
	Gln	Gly	Thr	Phe	Val	Asp	Asn	Leu	Ala	Leu	Asn	Lys	Gly	Gly	Ala	Leu	145	150	155	160
40	Tyr	Thr	Glu	Thr	Asn	Leu	Ser	Ile	Lys	Asp	Asn	Lys	Gly	Pro	Ile	Ile	165	170	175	
	Ile	Lys	Gln	Asn	Arg	Ala	Leu	Asn	Ser	Asp	Ser	Leu	Gly	Gly	Gly	Ile	180	185	190	
	Tyr	Ser	Gly	Asn	Ser	Leu	Asn	Ile	Glu	Gly	Asn	Ser	Gly	Ala	Ile	Gln	195	200	205	
50	Ile	Thr	Ser	Asn	Ser	Ser	Gly	Ser	Gly	Gly	Gly	Ile	Phe	Ser	Thr	Gln	210	215	220	
	Thr	Leu	Thr	Ile	Ser	Ser	Asn	Lys	Lys	Leu	Ile	Glu	Ile	Ser	Glu	Asn	225	230	235	240
	Ser	Ala	Phe	Ala	Asn	Asn	Tyr	Gly	Ser	Asn	Phe	Asn	Pro	Gly	Gly	Gly	245	250	255	
	Gly	Leu	Thr	Thr	Thr	Phe	Cys	Thr	Ile	Leu	Asn	Asn	Arg	Glu	Gly	Val	260	265	270	
60	Leu	Phe	Asn	Asn	Asn	Gln	Ser	Gln	Ser	Asn	Gly	Gly	Ala	Ile	His	Ala	275	280	285	

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	Lys	Ser	Ile	Ile	Ile	Lys	Glu	Asn	Gly	Pro	Val	Tyr	Phe	Leu	Asn	Asn	
	290						295					300					
	Thr	Ala	Thr	Arg	Gly	Gly	Ala	Leu	Leu	Asn	Leu	Ser	Ala	Gly	Ser	Gly	
	305					310					315					320	
10	Asn	Gly	Ser	Phe	Ile	Leu	Ser	Ala	Asp	Asn	Gly	Asp	Ile	Ile	Phe	Asn	
					325					330					335		
	Asn	Asn	Thr	Ala	Ser	Lys	His	Ala	Leu	Asn	Pro	Pro	Tyr	Arg	Asn	Ala	
				340					345					350			
	Ile	His	Ser	Thr	Pro	Asn	Met	Asn	Leu	Gln	Ile	Gly	Ala	Arg	Pro	Gly	
				355				360					365				
20	Tyr	Arg	Val	Leu	Phe	Tyr	Asp	Pro	Ile	Glu	His	Glu	Leu	Pro	Ser	Ser	
	370						375					380					
	Phe	Pro	Ile	Leu	Phe	Asn	Phe	Glu	Thr	Gly	His	Thr	Gly	Thr	Val	Leu	
	385					390					395					400	
	Phe	Ser	Gly	Glu	His	Val	His	Gln	Asn	Phe	Thr	Asp	Glu	Met	Asn	Phe	
					405					410					415		
	Phe	Ser	Tyr	Leu	Arg	Asn	Thr	Ser	Glu	Leu	Arg	Gln	Gly	Val	Leu	Ala	
				420					425					430			
30	Val	Glu	Asp	Gly	Ala	Gly	Leu	Ala	Cys	Tyr	Lys	Phe	Phe	Gln	Arg	Gly	
			435				440						445				
	Gly	Thr	Leu	Leu	Leu	Gly	Gln	Gly	Ala	Val	Ile	Thr	Thr	Ala	Gly	Thr	
		450					455					460					
	Ile	Pro	Thr	Pro	Ser	Ser	Thr	Pro	Thr	Thr	Val	Gly	Ser	Thr	Ile	Thr	
	465					470					475					480	
40	Leu	Asn	His	Ile	Ala	Ile	Asp	Leu	Pro	Ser	Ile	Leu	Ser	Phe	Gln	Ala	
					485				490						495		
	Gln	Ala	Pro	Lys	Ile	Trp	Ile	Tyr	Pro	Thr	Lys	Thr	Gly	Ser	Thr	Tyr	
				500					505					510			
	Thr	Glu	Asp	Ser	Asn	Pro	Thr	Ile	Thr	Ile	Ser	Gly	Thr	Leu	Thr	Leu	
			515					520					525				
50	Arg	Asn	Ser	Asn	Asn	Glu	Asp	Pro	Tyr	Asp	Ser	Leu	Asp	Leu	Ser	His	
	530						535					540					
	Ser	Leu	Glu	Lys	Val	Pro	Leu	Leu	Tyr	Ile	Val	Asp	Val	Ala	Ala	Gln	
	545					550					555					560	
	Lys	Ile	Asn	Ser	Ser	Gln	Leu	Asp	Leu	Ser	Thr	Leu	Asn	Ser	Gly	Glu	
					565					570					575		
	His	Tyr	Gly	Tyr	Gln	Gly	Ile	Trp	Ser	Thr	Tyr	Trp	Val	Glu	Thr	Thr	
				580				585						590			
60	Thr	Ile	Thr	Asn	Pro	Thr	Ser	Leu	Leu	Gly	Ala	Asn	Thr	Lys	His	Lys	
			595					600					605				

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	Leu	Leu	Tyr	Ala	Asn	Trp	Ser	Pro	Leu	Gly	Tyr	Arg	Pro	His	Pro	Glu
	610						615					620				
	Arg	Arg	Gly	Glu	Phe	Ile	Thr	Asn	Ala	Leu	Trp	Gln	Ser	Ala	Tyr	Thr
	625					630					635					640
10	Ala	Leu	Ala	Gly	Leu	His	Ser	Leu	Ser	Ser	Trp	Asp	Glu	Glu	Lys	Gly
					645					650					655	
	His	Ala	Ala	Ser	Leu	Gln	Gly	Ile	Gly	Leu	Leu	Val	His	Gln	Lys	Asp
				660					665					670		
	Lys	Asn	Gly	Phe	Lys	Gly	Phe	Arg	Ser	His	Met	Thr	Gly	Tyr	Ser	Ala
			675					680					685			
	Thr	Thr	Glu	Ala	Thr	Ser	Ser	Gln	Ser	Pro	Asn	Phe	Ser	Leu	Gly	Phe
		690					695					700				
20	Ala	Gln	Phe	Phe	Ser	Lys	Ala	Lys	Glu	His	Glu	Ser	Gln	Asn	Ser	Thr
	705					710					715					720
	Ser	Ser	His	His	Tyr	Phe	Ser	Gly	Met	Cys	Ile	Ala	Lys	Tyr	Ser	Leu
					725					730					735	
	Gln	Arg	Val	Ile	Arg	Leu	Ser	Val	Ser	Leu	Ala	Tyr	Met	Phe	Thr	Ser
				740					745					750		
30	Glu	His	Thr	His	Thr	Met	Tyr	Gln	Gly	Leu	Leu	Glu	Gly	Asn	Ser	Gln
			755					760					765			
	Gly	Ser	Phe	His	Asn	His	Thr	Leu	Ala	Gly	Ala	Leu	Ser	Cys	Val	Phe
		770					775					780				
	Leu	Pro	Gln	Pro	His	Gly	Glu	Ser	Leu	Gln	Ile	Tyr	Pro	Phe	Ile	Thr
	785					790					795					800
40	Ala	Leu	Ala	Ile	Arg	Gly	Asn	Leu	Ala	Ala	Phe	Gln	Glu	Ser	Gly	Asp
					805					810					815	
	His	Ala	Arg	Glu	Phe	Ser	Leu	His	Arg	Pro	Leu	Thr	Asp	Val	Ser	Leu
				820					825					830		
	Pro	Val	Gly	Ile	Arg	Ala	Ser	Trp	Lys	Asn	His	His	Arg	Val	Pro	Leu
			835					840					845			
	Val	Trp	Leu	Thr	Glu	Ile	Ser	Tyr	Arg	Ser	Thr	Leu	Tyr	Arg	Gln	Asp
		850					855					860				
50	Pro	Glu	Leu	His	Ser	Lys	Leu	Leu	Ile	Ser	Gln	Gly	Thr	Trp	Thr	Thr
	865					870					875					880
	Gln	Ala	Thr	Pro	Val	Thr	Tyr	Asn	Ala	Leu	Gly	Ile	Lys	Val	Lys	Asn
					885					890					895	
	Thr	Met	Gln	Val	Phe	Pro	Lys	Val	Thr	Leu	Ser	Leu	Asp	Tyr	Ser	Ala
				900					905					910		
60	Asp	Ile	Ser	Ser	Ser	Thr	Leu	Ser	His	Tyr	Leu	Asn	Val	Ala	Ser	Arg
			915					920					925			

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Met Arg Phe  
930

<210> 44  
<211> 978  
<212> PRT

10 <213> Chlamydia pneumoniae

<400> 44

Met Pro Leu Ser Phe Lys Ser Ser Ser Phe Cys Leu Leu Ala Cys Leu  
1 5 10 15

Cys Ser Ala Ser Cys Ala Phe Ala Glu Thr Arg Leu Gly Gly Asn Phe  
20 25 30

20 Val Pro Pro Ile Thr Asn Gln Gly Glu Glu Ile Leu Leu Thr Ser Asp  
35 40 45

Phe Val Cys Ser Asn Phe Leu Gly Ala Ser Phe Ser Ser Ser Phe Ile  
50 55 60

Asn Ser Ser Ser Asn Leu Ser Leu Leu Gly Lys Gly Leu Ser Leu Thr  
65 70 75 80

30 Phe Thr Ser Cys Gln Ala Pro Thr Asn Ser Asn Tyr Ala Leu Leu Ser  
85 90 95

Ala Ala Glu Thr Leu Thr Phe Lys Asn Phe Ser Ser Ile Asn Phe Thr  
100 105 110

Gly Asn Gln Ser Thr Gly Leu Gly Gly Leu Ile Tyr Gly Lys Asp Ile  
115 120 125

Val Phe Gln Ser Ile Lys Asp Leu Ile Phe Thr Thr Asn Arg Val Ala  
130 135 140

40 Tyr Ser Pro Ala Ser Val Thr Thr Ser Ala Thr Pro Ala Ile Thr Thr  
145 150 155 160

Val Thr Thr Gly Ala Ser Ala Leu Gln Pro Thr Asp Ser Leu Thr Val  
165 170 175

Glu Asn Ile Ser Gln Ser Ile Lys Phe Phe Gly Asn Leu Ala Asn Phe  
180 185 190

50 Gly Ser Ala Ile Ser Ser Ser Pro Thr Ala Val Val Lys Phe Ile Asn  
195 200 205

Asn Thr Ala Thr Met Ser Phe Ser His Asn Phe Thr Ser Ser Gly Gly  
210 215 220

Gly Val Ile Tyr Gly Gly Ser Ser Leu Leu Phe Glu Asn Asn Ser Gly  
225 230 235 240

Cys Ile Ile Phe Thr Ala Asn Ser Cys Val Asn Ser Leu Lys Gly Val  
245 250 255

60

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	Thr	Pro	Ser	Ser	Gly	Thr	Tyr	Ala	Leu	Gly	Ser	Gly	Gly	Ala	Ile	Cys	
				260					265					270			
	Ile	Pro	Thr	Gly	Thr	Phe	Glu	Leu	Lys	Asn	Asn	Gln	Gly	Lys	Cys	Thr	
			275					280					285				
10	Phe	Ser	Tyr	Asn	Gly	Thr	Pro	Asn	Asp	Ala	Gly	Ala	Ile	Tyr	Ala	Glu	
		290					295					300					
	Thr	Cys	Asn	Ile	Val	Gly	Asn	Gln	Gly	Ala	Leu	Leu	Leu	Asp	Ser	Asn	
	305					310					315					320	
	Thr	Ala	Ala	Arg	Asn	Gly	Gly	Ala	Ile	Cys	Ala	Lys	Val	Leu	Asn	Ile	
				325						330					335		
	Gln	Gly	Arg	Gly	Pro	Ile	Glu	Phe	Ser	Arg	Asn	Arg	Ala	Glu	Lys	Gly	
				340					345					350			
20	Gly	Ala	Ile	Phe	Ile	Gly	Pro	Ser	Val	Gly	Asp	Pro	Ala	Lys	Gln	Thr	
			355					360					365				
	Ser	Thr	Leu	Thr	Ile	Leu	Ala	Ser	Glu	Gly	Asp	Ile	Ala	Phe	Gln	Gly	
		370					375					380					
	Asn	Met	Leu	Asn	Thr	Lys	Pro	Gly	Ile	Arg	Asn	Ala	Ile	Thr	Val	Glu	
	385					390				395						400	
30	Ala	Gly	Gly	Glu	Ile	Val	Ser	Leu	Ser	Ala	Gln	Gly	Gly	Ser	Arg	Leu	
					405					410					415		
	Val	Phe	Tyr	Asp	Pro	Ile	Thr	His	Ser	Leu	Pro	Thr	Thr	Ser	Pro	Ser	
				420					425					430			
	Asn	Lys	Asp	Ile	Thr	Ile	Asn	Ala	Asn	Gly	Ala	Ser	Gly	Ser	Val	Val	
			435					440					445				
40	Phe	Thr	Ser	Lys	Gly	Leu	Ser	Ser	Thr	Glu	Leu	Leu	Leu	Pro	Ala	Asn	
	450						455					460					
	Thr	Thr	Thr	Ile	Leu	Leu	Gly	Thr	Val	Lys	Ile	Ala	Ser	Gly	Glu	Leu	
	465				470						475					480	
	Lys	Ile	Thr	Asp	Asn	Ala	Val	Val	Asn	Val	Ala	Gly	Phe	Ala	Thr	Gln	
					485				490						495		
	Gly	Ser	Gly	Gln	Leu	Thr	Leu	Gly	Ser	Gly	Gly	Thr	Leu	Gly	Leu	Ala	
				500					505					510			
50	Thr	Pro	Thr	Gly	Ala	Pro	Ala	Ala	Val	Asp	Phe	Thr	Ile	Gly	Lys	Leu	
			515					520					525				
	Ala	Phe	Asp	Pro	Phe	Ser	Phe	Leu	Lys	Arg	Asp	Phe	Val	Ser	Ala	Ser	
		530					535					540					
	Val	Asn	Ala	Gly	Thr	Lys	Asn	Val	Thr	Leu	Thr	Gly	Ala	Leu	Val	Leu	
	545					550					555					560	
60	Asp	Glu	His	Asp	Val	Thr	Asp	Leu	Tyr	Asp	Met	Val	Ser	Leu	Gln	Ser	
					565					570					575		

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	Pro	Val	Ala	Ile	Pro	Ile	Ala	Val	Phe	Lys	Gly	Ala	Thr	Val	Thr	Lys	
				580					585					590			
	Thr	Gly	Phe	Pro	Asp	Gly	Glu	Ile	Ala	Thr	Pro	Ser	His	Tyr	Gly	Tyr	
			595					600					605				
10	Gln	Gly	Lys	Trp	Ser	Tyr	Thr	Trp	Ser	Arg	Pro	Leu	Leu	Ile	Pro	Ala	
		610					615					620					
	Pro	Asp	Gly	Gly	Phe	Pro	Gly	Gly	Pro	Ser	Pro	Ser	Ala	Asn	Thr	Leu	
	625					630					635					640	
	Tyr	Ala	Val	Trp	Asn	Ser	Asp	Thr	Leu	Val	Arg	Ser	Thr	Tyr	Ile	Leu	
					645					650					655		
	Asp	Pro	Glu	Arg	Tyr	Gly	Glu	Ile	Val	Ser	Asn	Ser	Leu	Trp	Ile	Ser	
20				660					665					670			
	Phe	Leu	Gly	Asn	Gln	Ala	Phe	Ser	Asp	Ile	Leu	Gln	Asp	Val	Leu	Leu	
			675					680					685				
	Ile	Asp	His	Pro	Gly	Leu	Ser	Ile	Thr	Ala	Lys	Ala	Leu	Gly	Ala	Tyr	
		690					695					700					
	Val	Glu	His	Thr	Pro	Arg	Gln	Gly	His	Glu	Gly	Phe	Ser	Gly	Arg	Tyr	
	705					710					715					720	
30	Gly	Gly	Tyr	Gln	Ala	Ala	Leu	Ser	Met	Asn	Tyr	Thr	Asp	His	Thr	Thr	
				725						730					735		
	Leu	Gly	Leu	Ser	Phe	Gly	Gln	Leu	Tyr	Gly	Lys	Thr	Asn	Ala	Asn	Pro	
				740					745					750			
	Tyr	Asp	Ser	Arg	Cys	Ser	Glu	Gln	Met	Tyr	Leu	Leu	Ser	Phe	Phe	Gly	
			755					760					765				
40	Gln	Phe	Pro	Ile	Val	Thr	Gln	Lys	Ser	Glu	Ala	Leu	Ile	Ser	Trp	Lys	
		770					775					780					
	Ala	Ala	Tyr	Gly	Tyr	Ser	Lys	Asn	His	Leu	Asn	Thr	Thr	Tyr	Leu	Arg	
	785					790					795					800	
	Pro	Asp	Lys	Ala	Pro	Lys	Ser	Gln	Gly	Gln	Trp	His	Asn	Asn	Ser	Tyr	
					805					810					815		
	Tyr	Val	Leu	Ile	Ser	Ala	Glu	His	Pro	Phe	Leu	Asn	Trp	Cys	Leu	Leu	
				820					825					830			
50	Thr	Arg	Pro	Leu	Ala	Gln	Ala	Trp	Asp	Leu	Ser	Gly	Phe	Ile	Ser	Ala	
				835				840						845			
	Glu	Phe	Leu	Gly	Gly	Trp	Gln	Ser	Lys	Phe	Thr	Glu	Thr	Gly	Asp	Leu	
		850					855					860					
	Gln	Arg	Ser	Phe	Ser	Arg	Gly	Lys	Gly	Tyr	Asn	Val	Ser	Leu	Pro	Ile	
	865					870					875					880	
60	Gly	Cys	Ser	Ser	Gln	Trp	Phe	Thr	Pro	Phe	Lys	Lys	Ala	Pro	Ser	Thr	
					885					890					895		



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Leu Thr Ile Lys Leu Ala Tyr Lys Pro Asp Ile Tyr Arg Val Asn Pro  
                   900                                  905                                  910

His Asn Ile Val Thr Val Val Ser Asn Gln Glu Ser Thr Ser Ile Ser  
                   915                                  920                                  925

10 Gly Ala Asn Leu Arg Arg His Gly Leu Phe Val Gln Ile His Asp Val  
                   930                                  935                                  940

Val Asp Leu Thr Glu Asp Thr Gln Ala Phe Leu Asn Tyr Thr Phe Asp  
   945                                  950                                  955                                  960

Gly Lys Asn Gly Phe Thr Asn His Arg Val Ser Thr Gly Leu Lys Ser  
                   965                                  970                                  975

Thr Phe

20 <210> 45  
       <211> 813  
       <212> PRT  
       <213> Chlamydia pneumoniae

      <400> 45  
 Ser Ala Leu Gln Pro Thr Asp Ser Leu Thr Val  
   1                                  5                                  10

30 Glu Asn Ile Ser Gln Ser Ile Lys Phe Phe Gly Asn Leu Ala Asn Phe  
                   15                                  20                                  25

Gly Ser Ala Ile Ser Ser Ser Pro Thr Ala Val Val Lys Phe Ile Asn  
                   30                                  35                                  40

Asn Thr Ala Thr Met Ser Phe Ser His Asn Phe Thr Ser Ser Gly Gly  
                   45                                  50                                  55

40 Gly Val Ile Tyr Gly Gly Ser Ser Leu Leu Phe Glu Asn Asn Ser Gly  
                   60                                  65                                  70                                  75

Cys Ile Ile Phe Thr Ala Asn Ser Cys Val Asn Ser Leu Lys Gly Val  
                   80                                  85                                  90

Thr Pro Ser Ser Gly Thr Tyr Ala Leu Gly Ser Gly Gly Ala Ile Cys  
                   95                                  100                                  105

Ile Pro Thr Gly Thr Phe Glu Leu Lys Asn Asn Gln Gly Lys Cys Thr  
                   110                                  115                                  120

50 Phe Ser Tyr Asn Gly Thr Pro Asn Asp Ala Gly Ala Ile Tyr Ala Glu  
                   125                                  130                                  135

Thr Cys Asn Ile Val Gly Asn Gln Gly Ala Leu Leu Leu Asp Ser Asn  
   140                                  145                                  150                                  155

Thr Ala Ala Arg Asn Gly Gly Ala Ile Cys Ala Lys Val Leu Asn Ile  
                   160                                  165                                  170

60 Gln Gly Arg Gly Pro Ile Glu Phe Ser Arg Asn Arg Ala Glu Lys Gly  
                   175                                  180                                  185

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	Gly	Ala	Ile	Phe	Ile	Gly	Pro	Ser	Val	Gly	Asp	Pro	Ala	Lys	Gln	Thr	
			190					195					200				
	Ser	Thr	Leu	Thr	Ile	Leu	Ala	Ser	Glu	Gly	Asp	Ile	Ala	Phe	Gln	Gly	
		205					210					215					
10	Asn	Met	Leu	Asn	Thr	Lys	Pro	Gly	Ile	Arg	Asn	Ala	Ile	Thr	Val	Glu	
		220				225					230					235	
	Ala	Gly	Gly	Glu	Ile	Val	Ser	Leu	Ser	Ala	Gln	Gly	Gly	Ser	Arg	Leu	
					240					245					250		
	Val	Phe	Tyr	Asp	Pro	Ile	Thr	His	Ser	Leu	Pro	Thr	Thr	Ser	Pro	Ser	
				255					260					265			
	Asn	Lys	Asp	Ile	Thr	Ile	Asn	Ala	Asn	Gly	Ala	Ser	Gly	Ser	Val	Val	
20			270					275					280				
	Phe	Thr	Ser	Lys	Gly	Leu	Ser	Ser	Thr	Glu	Leu	Leu	Leu	Pro	Ala	Asn	
		285					290					295					
	Thr	Thr	Thr	Ile	Leu	Leu	Gly	Thr	Val	Lys	Ile	Ala	Ser	Gly	Glu	Leu	
		300			305						310					315	
	Lys	Ile	Thr	Asp	Asn	Ala	Val	Val	Asn	Val	Ala	Gly	Phe	Ala	Thr	Gln	
					320					325					330		
30	Gly	Ser	Gly	Gln	Leu	Thr	Leu	Gly	Ser	Gly	Gly	Thr	Leu	Gly	Leu	Ala	
				335				340						345			
	Thr	Pro	Thr	Gly	Ala	Pro	Ala	Ala	Val	Asp	Phe	Thr	Ile	Gly	Lys	Leu	
			350					355					360				
	Ala	Phe	Asp	Pro	Phe	Ser	Phe	Leu	Lys	Arg	Asp	Phe	Val	Ser	Ala	Ser	
		365					370					375					
40	Val	Asn	Ala	Gly	Thr	Lys	Asn	Val	Thr	Leu	Thr	Gly	Ala	Leu	Val	Leu	
		380				385					390					395	
	Asp	Glu	His	Asp	Val	Thr	Asp	Leu	Tyr	Asp	Met	Val	Ser	Leu	Gln	Ser	
					400					405					410		
	Pro	Val	Ala	Ile	Pro	Ile	Ala	Val	Phe	Lys	Gly	Ala	Thr	Val	Thr	Lys	
				445					420					425			
	Thr	Gly	Phe	Pro	Asp	Gly	Glu	Ile	Ala	Thr	Pro	Ser	His	Tyr	Gly	Tyr	
50			430				435						440				
	Gln	Gly	Lys	Trp	Ser	Tyr	Thr	Trp	Ser	Arg	Pro	Leu	Leu	Ile	Pro	Ala	
		445					450					455					
	Pro	Asp	Gly	Gly	Phe	Pro	Gly	Gly	Pro	Ser	Pro	Ser	Ala	Asn	Thr	Leu	
		460				465					470					475	
	Tyr	Ala	Val	Trp	Asn	Ser	Asp	Thr	Leu	Val	Arg	Ser	Thr	Tyr	Ile	Leu	
					480				485						490		
60	Asp	Pro	Glu	Arg	Tyr	Gly	Glu	Ile	Val	Ser	Asn	Ser	Leu	Trp	Ile	Ser	
				495					500					505			

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60